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OM protein - protein search, using sw model		13	399	59.1	132	20	AAW82403
Run on:	January 24, 2002, 09:08:13 ; Search time 23.82 Seconds (without alignments) 410.482 Million cell updates/sec	14	396	58.7	117	21	AAQ03847
Title:	US-09-905-235-1	15	386.5	57.3	131	22	AAQ65580
Perfect score:	675	16	382	56.6	132	21	AAQ03957
Sequence:	1 MCDAFVGTWKLSSENFFDDY.KLVVECYMKGVNSTRVYERA 132	17	381	56.4	132	16	AAR75423
Scoring table:	BLOSUM62	18	375	55.6	88	21	AAB8740
	Gapop 10.0 , Gapext 0.5	19	366	54.2	135	15	AAR5866
Searched:	522463 seqs, 7407320 residues	20	360	53.3	82	22	AAG75123
Total number of hits satisfying chosen parameters:	522463	21	270	40.0	69	21	AAY65303
Minimum DB seq length: 0		22	237	35.1	134	20	AHW8550
Maximum DB seq length: 2000000000		23	229.5	34.0	133	16	AAR75643
Post-processing: Minimum Match 0%		24	222	32.9	137	14	AAR42212
	Maximum Match 100%	25	210	31.1	56	21	AAU01405
Scoring table:	BLOSUM62	26	201.5	29.9	138	14	AAR42211
	Gapop 10.0 , Gapext 0.5	27	201.5	29.9	138	22	AAB76852
Searched:	522463 seqs, 7407320 residues	28	201.5	29.9	149	21	AAE81158
Total number of hits satisfying chosen parameters:	522463	29	194	28.7	99	21	AAQ01603
Minimum DB seq length: 0		30	186	27.6	160	21	AAB43403
Maximum DB seq length: 2000000000		31	165	24.4	135	22	AAM38758
Post-processing: Minimum Match 0%		32	165	24.4	135	22	AAB60559
	Maximum Match 100%	33	165	24.4	168	22	AAM40544
Scoring table:	BLOSUM62	34	164	24.3	135	18	AAM30891
	Gapop 10.0 , Gapext 0.5	35	164	24.3	135	20	AAY32504
Searched:	522463 seqs, 7407320 residues	36	164	24.3	135	22	AAG66575
Total number of hits satisfying chosen parameters:	522463	37	164	24.3	135	22	AAU02203
Minimum DB seq length: 0		38	162	24.0	135	21	AAY92910
Maximum DB seq length: 2000000000		39	136	20.1	156	22	AAU02202
Post-processing: Minimum Match 0%		40	122	18.1	107	18	AHW75561
	Maximum Match 100%	41	122	18.1	107	18	AHW6581
Scoring table:	A_Geneseq_1101:*	42	122	18.1	107	20	AAY49535
	1: /SIDSB8/gcadata/geneseq/geneseqP/AA1980.DAT:*	43	122	18.1	107	20	AHW3929
Searched:	522463 seqs, 7407320 residues	44	115.5	17.1	106	22	AAG66579
Total number of hits satisfying chosen parameters:	522463	45	110	16.3	55	9	AAP82557

ALIGNMENTS

Database :	A_Geneseq_1101:*	RESULT 1
	1: /SIDSB8/gcadata/geneseq/geneseqP/AA1980.DAT:*	AAU90320
	2: /SIDSB8/gcadata/geneseq/geneseqP/AA1981.DAT:*	ID AAY90320 standard; Protein; 132 AA.
	3: /SIDSB8/gcadata/geneseq/geneseqP/AA1982.DAT:*	XX
	4: /SIDSB8/gcadata/geneseq/geneseqP/AA1983.DAT:*	XX
	5: /SIDSB8/gcadata/geneseq/geneseqP/AA1984.DAT:*	AC AAY90320;
	6: /SIDSB8/gcadata/geneseq/geneseqP/AA1985.DAT:*	XX
	7: /SIDSB8/gcadata/geneseq/geneseqP/AA1986.DAT:*	DT 22-NOV-2000 (first entry)
	8: /SIDSB8/gcadata/geneseq/geneseqP/AA1987.DAT:*	XX
	9: /SIDSB8/gcadata/geneseq/geneseqP/AA1988.DAT:*	DE Human AFABP protein sequence.
	10: /SIDSB8/gcadata/geneseq/geneseqP/AA1989.DAT:*	XX
	11: /SIDSB8/gcadata/geneseq/geneseqP/AA1990.DAT:*	XX
	12: /SIDSB8/gcadata/geneseq/geneseqP/AA1991.DAT:*	XX
	13: /SIDSB8/gcadata/geneseq/geneseqP/AA1992.DAT:*	XX
	14: /SIDSB8/gcadata/geneseq/geneseqP/AA1993.DAT:*	XX
	15: /SIDSB8/gcadata/geneseq/geneseqP/AA1994.DAT:*	XX
	16: /SIDSB8/gcadata/geneseq/geneseqP/AA1995.DAT:*	XX
	17: /SIDSB8/gcadata/geneseq/geneseqP/AA1996.DAT:*	XX
	18: /SIDSB8/gcadata/geneseq/geneseqP/AA1997.DAT:*	XX
	19: /SIDSB8/gcadata/geneseq/geneseqP/AA1998.DAT:*	XX
	20: /SIDSB8/gcadata/geneseq/geneseqP/AA1999.DAT:*	XX
	21: /SIDSB8/gcadata/geneseq/geneseqP/AA2000.DAT:*	KW AFABP; adipocyte fatty acid binding protein; atherosclerotic lesion; KW lesion formation inhibition; macrophage; adipocyte; atherosclerosis; KW serum cholesterol; therapy; human.
	22: /SIDSB8/gcadata/geneseq/geneseqP/AA2001.DAT:*	XX
		OS Homo sapiens.
		XX PN WO2000047734-A1.
		XX PN WO2000047734-A1.

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	675	100.0	132	21	ARY90320	Human AFABP protein
2	625	92.6	132	21	ARY90319	Mouse AFABP protein
3	466	69.0	133	22	AAG66576	Mouse MDG1 polypep
4	458	67.9	136	19	ARW40227	Human myelin P2 pr
5	453	67.1	131	12	AAR13559	MDG1 active peptide
6	449	66.5	133	22	AAG66578	Human MDG1 polypep
7	446	66.1	133	22	AAG66577	Bovine MDG1 polype
8	445	65.9	136	19	ARW40228	Bovine myelin P2 P
9	435.5	64.5	134	18	AAY31554	Porcine heart fatt
10	399	59.1	132	18	AAW22408	Human cytostatin I
11	399	59.1	132	19	AAW80949	Amino acid sequenc

N-PSDB; AAY37717.
Reducing expression of adipocyte fatty acid binding protein through administration of a compound is used to inhibit formation of an atherosclerotic lesion.

XX Disclosure; Page 14; 43PP; English.
 PS
 XX This sequence represents the human AFABP (adipocyte fatty acid binding protein) protein sequence. The invention relates to a method for inhibiting formation of an atherosclerotic lesion comprising administering to a mammal a compound that reduces expression of adipocyte fatty acid binding protein (AFABP). The method is used to inhibit formation of atherosclerotic lesions. The method is used to identify compounds which can be used to inhibit formation of atherosclerotic lesions through inhibition of AFABP binding to an intracellular ligand in a macrophage or adipocyte, inhibition of development of an atherosclerotic lesion, inhibition of a macrophage differentiating into a foam cell or inhibition of AFABP expression in a cell. AFABP activity may be inhibited to treat atherosclerosis or to treat individuals at risk of developing atherosclerosis. Inhibiting AFABP expression or activity reduces the development of atherosclerotic lesions despite a high level of serum cholesterol.
 XX Sequence 132 AA;
 SQ

Query Match Score 675; DB 21; Length 132;
 Best Local Similarity 100.0%; Pred. No. 4.2e-71;
 Matches 0; Mismatches 0; Indels 0; Gaps 0;
 CC
 Qy 1 MCDAFVGTVKLVSSSENNDDYMKKEYVGENTRKVAGMAKDNMISYNGDVITIKSESTFKN 60
 Db 1 mcdafvgtvklvssenfdyymkkeyvgfatrkvagmakdnmisyngdvtiksestfn 60
 Qy 61 TEISFLQGQEDEVTAADRKVKSTTLDGVLYHQWDGKSTTIKRKEDDKLVVECYM 120
 Db 61 teisflqgqeadevaddrkvssttldgvlyhqwdgksttikrkeddklvvecym 120
 Qy 121 KGVTSRVERA 132
 Db 121 kgtvstrvera 132
 XX

RESULT 2
 AAY90319
 ID AAY90319 standard; Protein: 132 AA.
 XX
 AC AAY90319;
 XX
 DT 22-NOV-2000 (first entry)
 DE Mouse AFABP protein sequence.
 XX
 KW AFABP; adipocyte fatty acid binding protein; atherosclerotic lesion; KW lesion formation inhibition; macrophage; adipocyte; atherosclerosis; KW serum cholesterol; therapy; mouse.
 XX
 OS Mus sp.
 XX
 PN WO200047734-A1.
 XX
 PD 17-AUG-2000.
 XX
 PF 11-FEB-2000; 2000WO-US03560.
 XX
 PR 12-FEB-1999; 99US-0119880.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Lee M, Perrella MA, Hotamisligil GS;
 XX
 DR WPI; 2000-50609/45.
 XX
 N-PSDE; AAA37716.
 XX
 Reducing expression of adipocyte fatty acid binding protein through PT administration of a compound is used to inhibit formation of an atherosclerotic lesion -

XX Disclosure; Page 14; 43PP; English.
 PS
 XX This sequence represents the mouse AFABP (adipocyte fatty acid binding protein) protein sequence. The invention relates to a method for inhibiting formation of an atherosclerotic lesion comprising administering to a mammal a compound that reduces expression of adipocyte fatty acid binding protein (AFABP). The method is used to inhibit formation of atherosclerotic lesions. The method is used to identify compounds which can be used to inhibit formation of atherosclerotic lesions through inhibition of AFABP binding to an intracellular ligand in a macrophage or adipocyte, inhibition of development of an atherosclerotic lesion, inhibition of a macrophage differentiating into a foam cell or inhibition of AFABP expression in a cell. AFABP activity may be inhibited to treat atherosclerosis or to treat individuals at risk of developing atherosclerosis. Inhibiting AFABP expression or activity reduces the development of atherosclerotic lesions despite a high level of serum cholesterol.
 XX Sequence 132 AA;

Query Match Score 625; DB 21; Length 132;
 Best Local Similarity 91.7%; Pred. No. 2.9e-65;
 Matches 121; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
 CC
 Qy 1 MCDAFVGTVKLVSSSENNDDYMKKEYVGENTRKVAGMAKDNMISYNGDVITIKSESTFKN 60
 Db 1 mcdafvgtvklvssenfdyymkkeyvgfatrkvagmakdnmisyngdvtiksestfn 60
 Qy 61 TEISFLQGQEDEVTAADRKVKSTTLDGVLYHQWDGKSTTIKRKEDDKLVVECYM 120
 Db 61 teisflqgqeadevaddrkvssttldgvlyhqwdgksttikrkeddklvvecym 120
 Qy 121 KGVTSRVERA 132
 Db 121 kgtvstrvera 132
 XX

RESULT 3
 AAG66576
 ID AAG66576 standard; Protein: 133 AA.
 XX
 AC AAG66576;
 XX
 DT 22-OCT-2001 (first entry)
 DE Mouse MDG1 polypeptide.
 XX
 KW Mouse; cytostatin III; cytotatic; epithelial cell growth; KW milk production; breast involution; cardiac myocyte hypertrophy; KW leukemia; MDG1; mammary-derived growth inhibitor.
 XX
 OS Mus sp.
 XX
 PN US622291-B1.
 XX
 PD 15-MAY-2001.
 XX
 PF 10-MAY-1999; 99US-0307817.
 XX
 PR 19-MAR-1996; 96US-013655.
 PR 19-MAR-1997; 97US-082025.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI N1 J, Yu G, Gentz R, Dillon PJ;
 XX
 DR WPI; 2001-342775/36.
 XX
 CYtostatin III polypeptides that modulate growth of epithelial cells, PT stimulate milk production in humans and cows and promote involution of PT breast, for research, biological, clinical and therapeutic purposes -

PT	Gullian-Barre syndrome
XX	
PS	Disclosure; Fig 2; 31pp; English.
XX	
CC	The invention relates to an isolated Cytostatin III polypeptide comprising a sequence selected from amino acids 1-135, 2-135, 108-135, 129-135 and 118-125 of a sequence of 135 amino acids fully defined in the specification. The polypeptide is useful for modulating growth of epithelial cells, for stimulating milk production in humans and cows, and for promoting involution of breasts. It is also useful for treating cardiac myocyte hypertrophy and leukaemia, and is useful for research, and biological, clinical and therapeutic purposes. The present sequence is provided in the specification for comparison studies with human cytostatin III.
XX	
Sequence	133 AA;
Query Match	69.0%; Score 466; DB 22; Length 133;
Best Local Similarity	67.9%; pred. No. 1.1e-16;
Matches	89; Conservative 15; Mismatches 27; Indels 0; Gaps 0;
QY	1 MCDAFVGTVKLVSSENFDVYMEKEYGVFAFRKVAGNAKPMNIISYNGDVITIKSESTEFKN 60
Db	1 madafvgtvklnsfddkmksyqfgrqasnrkptilexngdtitkifkn 60
QY	61 TEISFILGQEFDEVADDRKVKSITILDGGYLHYOKWDGKSTTIKRKRREDDKLVYECVM 120
Db	61 teisfklgefeettadhrktksivtqrgslinqvgrwdgkettikrklyngkmvaekcm 120
QY	121 KGVTSTRYE 130
Db	121 kgvvtctryd 130
RESULT	5
ID	AARI3559 standard; protein; 131 AA.
XX	
AC	AARI3559;
XX	
AAW40227	AAW40227 standard; Protein; 136 AA.
XX	
AAW40227;	
XX	
26-JUN-1998	(first entry)
XX	
Human myelin P2 protein.	
XX	
Human; myelin; P2 protein; treatment; inflammatory polyneuritis; Guillain-Barre syndrome; vasculitis; nerve inflammation; gammopathy.	
XX	
Homo sapiens.	
XX	
Key Misc-difference 49	Location/Qualifiers
FFFT	/note= "Encoded by AAT"
XX	
WO9803667-A2.	
XX	
29-JAN-1998.	
XX	
18-JUL-1997;	97NO-DE01535.
XX	
(GOLD/) (WEIS/)	GOLD R. WEISHAUPt A.
XX	
Gold R,	Weishaupt A;
XX	
WPI:	1998-120772/11.
DR	
N-PSDB;	AAV10405.
XX	
Recombinant myelin proteins for treating T-cell mediated disease of peripheral nervous system by high dose antigen therapy, causing apoptosis in T cells, for treating e.g. polyneuritis or Guillain-Barre syndrome, vasculitis and nerve inflammation in cases of gammopathy.	
PT	
PT	Mammary-derived Growth Inhibitor peptide(s) - and antibodies useful in biotechnology and medicine as proliferation inhibitors e.g. of carcinoma cells
XX	
PS	Disclosure; Page 2; 6pp; German.
XX	
Query Match	67.9%; Score 458; DB 19; Length 136;
Best Local Similarity	66.3%; pred. No. 1e-45;
Matches	87; Conservative 17; Mismatches 26; Indels 0; Gaps
QY	1 MCDAFVGTVKLVSSENFDVYMEKEYGVFAFRKVAGNAKPMNIISYNGDVITIKSESTEFKN 60
Db	1 msnkflgtnklnsfddkmksyqfgrqasnrkptilexngdtitkifkn 60
QY	61 TEISFILGQEFDEVADDRKVKSITILDGGYLHYOKWDGKSTTIKRKRREDDKLVYECVM 120
Db	61 teisfklgefeettadhrktksivtqrgslinqvgrwdgkettikrklyngkmvaekcm 120
QY	121 KGVTSTRYE 130
Db	121 kgvvtctryd 130
RESULT	5
ID	AARI3559
XX	
AC	AARI3559;
XX	
AAW40227;	
XX	
26-NOV-1991	(first entry)
XX	
MDGI active peptides.	
XX	
KW	Proliferation; inhibition; mammary-derived growth inhibitor.
XX	
OS	Synthetic.
XX	
FH	Key Peptide
FT	69-78
FT	Location/Qualifiers
FT	/label= "active_peptide
FT	/note= "claim 10"
FT	121-131
FT	/label= "active_peptide
FT	/note= "claim 11"
XX	
PN	DE4005062-A.
XX	
PD	22-AUG-1991.
XX	
PF	15-FEB-1990;
XX	
PR	15-FEB-1990;
XX	
PA	(GROS/) GROSSE R.
XX	
PI	Grosse R, Langen P, Bohmer FD, Wallukat G;
XX	
DR	WP1: 1991-251439/35.
XX	
PT	Mammary-derived Growth Inhibitor peptide(s) - and antibodies useful in biotechnology and medicine as proliferation inhibitors e.g. of carcinoma cells
CC	The indicated nentides and the nentides represented in AAV10405 and

CC AAR13561 are used for the production of antibodies. These are used to
 CC study the mechanism of action of MDGI and related proteins and to
 CC identify new regulators active in the same way.
 CC The peptides are synthesised by usual chemical methods and coupled
 CC to a carrier. The resulting conjugate is used to immunise animals
 CC and recovered sera tested for reactivity against antigens
 CC immobilised on nitrocellulose.

XX Sequence 131 AA;

Query Match 67.1%; Score 453; DB 12; Length 131;
 Best Local Similarity 67.4%; Pred. No. 3.7e-45; Gaps 0;
 Matches 87; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

Qy 3 DAFVGTWKLVSENFDYMDKMEVGFEATRKGAGNAKPNNITSYNGDVITIKSESTEFKNE 62
 Db 2 dafvgtwkvlvsenfdydmkslgvfrqgntkptliisngdtvilktsfknke 61

Qy 63 ISFILGQEQEDEVTADDRKVTKSTINTLDGGVLVHVKWDGKSTIKRKREDDKLVVECYNKG 122
 Db 62 isfklgverdettaddrkvtkstintldggvlvhqkwdgqetttvrlidgkivhlgkwdgqetttvrlidgklltgh 121

Qy 123 VTSTRYER 131
 Db 122 avctryek 130

RESULT 6

AAG66578 standard; Protein; 133 AA.

AC AAG66578;

XX 22-OCT-2001 (first entry)

XX DT 22-OCT-2001 (first entry)

XX DE Bovine MDGI polypeptide.

XX AC Bovine; cytostatin III; cytostatic; epithelial cell growth;

XX KW milk production; breast involution; cardiac myocyte hypertrophy;

XX KW leukaemia; MDGI; mammary-derived growth inhibitor.

XX OS Bos sp.

XX PN US6232291-B1.

XX PD 15-MAY-2001.

XX PF 10-MAY-1999; 99US-0307817.

XX PR 19-MAR-1996; 96US-0013655.

XX PR 15-MAY-2001.

XX PR 10-MAY-1999; 99US-0307817.

XX PR 19-MAR-1996; 96US-0013655.

XX PR 19-MAR-1997; 97US-0820625.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ni J, Yu G, Gentz R, Dillon PJ;

XX DR WPI; 2001-342775/36.

XX PS Disclosure; Fig 2; 31pp; English.

XX PT Cytostatin III polypeptides that modulate growth of epithelial cells,

XX PT stimulate milk production in humans and cows and promote involution of

XX PT breast, for research, biological, clinical and therapeutic purposes -

XX Disclosure; Fig 2; 31pp; English.

XX PT Cytostatin III polypeptides that modulate growth of epithelial cells,

XX PT stimulate milk production in humans and cows and promote involution of

XX PT breast, for research, biological, clinical and therapeutic purposes -

XX Disclosure; Fig 2; 31pp; English.

XX PT The invention relates to an isolated Cytostatin III polypeptide,

XX comprising a sequence selected from amino acids 1-135, 2-135, 108-135,

XX 129-135 and 118-125, of a sequence of 135 amino acids fully defined in

XX the specification. The polypeptide is useful for modulating growth of

XX epithelial cells, for stimulating milk production in humans and cows,

XX and for promoting involution of breasts. It is also useful for treating,

XX cardiac myocyte hypertrophy and leukaemia, and is useful for research,

XX and biological, clinical and therapeutic purposes. The present

CC sequence is provided in the specification for comparison studies

CC with human cytostatin III.

CC Sequence 133 AA;

Query Match 66.5%; Score 449; DB 22; Length 133;
 Best Local Similarity 64.9%; Pred. No. 1.1e-44;
 Matches 85; Conservative 16; Mismatches 30; Indels 0; Gaps 0;

Qy 1 MCDAFVGTVKLVYSSENFDYMDKMEVGFEATRKGAGNAKPNNITSYNGDVITIKSESTEFKNE 60
 Db 1 mvaflgwkvlvsenfdydmkslgvfrqgntkptliisngdtvilktsfknke 60

Qy 61 TEISFILGQEQEDEVTADDRKVTKSTINTLDGGVLVHVKWDGKSTIKRKREDDKLVVECYM 120
 Db 61 teisfklgverdettaddrkvtkstintldggvlvhqkwdgqetttvrlidgkivhlgkwdgqetttvrlidgklltgh 120

Qy 121 KGVTSTRYER 131
 Db 121 gtavcrttylek 131

RESULT 7

ID AAG66577 standard; Protein; 133 AA.

XX AAG66577;

AC AAG66577;

XX 22-OCT-2001 (first entry)

XX DE Bovine MDGI polypeptide.

XX AC Bovine; cytostatin III; cytostatic; epithelial cell growth;

XX KW milk production; breast involution; cardiac myocyte hypertrophy;

XX KW leukaemia; MDGI; mammary-derived growth inhibitor.

XX OS Bos sp.

XX PN US6232291-B1.

XX PD 15-MAY-2001.

XX PF 10-MAY-1999; 99US-0307817.

XX PR 19-MAR-1996; 96US-0013655.

XX PR 19-MAR-1997; 97US-0820825.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PI Ni J, Yu G, Gentz R, Dillon PJ;

XX DR WPI; 2001-342775/36.

XX PS Disclosure; Fig 2; 31pp; English.

XX PT Cytostatin III polypeptides that modulate growth of epithelial cells,

XX PT stimulate milk production in humans and cows and promote involution of

XX PT breast, for research, biological, clinical and therapeutic purposes -

XX Disclosure; Fig 2; 31pp; English.

XX PT The invention relates to an isolated Cytostatin III polypeptide,

XX comprising a sequence selected from amino acids 1-135, 2-135, 108-135,

XX 129-135 and 118-125, of a sequence of 135 amino acids fully defined in

XX the specification. The polypeptide is useful for modulating growth of

XX epithelial cells, for stimulating milk production in humans and cows,

XX and for promoting involution of breasts. It is also useful for treating,

XX cardiac myocyte hypertrophy and leukaemia, and is useful for research,

XX and biological, clinical and therapeutic purposes. The present

CC sequence is provided in the specification for comparison studies

CC with human cytostatin III.

XX Sequence 133 AA;

Query Match	66.1%	Score 446;	DB 22;	Length 133;	QY	61 TEISFILGQEFDEVTTADDRKVKSTTLDGGVLVHVKWKGKSTTIRKREDDKLVYRCVM 120
Best Local Similarity	64.9%	Pred. No. 2.5e-44;	Matches 15;	Indels 0;	Db	61 teisfkgqefettadnrktstvtlargsinqvqwdgnettikrlvngkmvveckm 120
Matches 85; Conservative			Mismatches 31;	Gaps 0;	QY	1 MCDAFGVGTWKLYSSENFDYYMKVEGVGPATRKVAGMAKPNMIIISVNGDVTIKSESTFKN 60
Db	1 mvdafgtwklvdsknfodymkslgvgfatrgnmtkpttlevngdtvilkqtstfkn 60				Db	121 KGITSTRYVE 130
QY	61 TEISFILGQEFDEVTTADDRKVKSTTLDGGVLVHVKWKGKSTTIRKREDDKLVYRCVM 120				QY	121 KGITSTRYVE 130
Db	61 teisfkgqefettadnrktstvtlargsinqvqwdgnettikrlvngkmvveckm 120				Db	121 kdvtctiyd 130
QY	121 KGITSTRYVE 131				RESULT 9	
Db	121 gtavctrtyek 131				ID AAW31534	AAW31534 standard; Protein; 134 AA.
QY	121 KGITSTRYVE 131				XX	AAW31534;
Db	121 gtavctrtyek 131				AC	AAW31534;
RESULT 8					DT	20-APR-1998 (first entry)
ID AAW40228					DE	Porcine heart-fatty acid binding protein.
XX					XX	KW Porcine; pig; swine; heart-fatty acid binding protein; H-FABP;
ID AAW40228 standard; Protein; 136 AA.					XX	KW localisation; identification; marking; gene; allele;
AC AAW40228;					XX	KW quantitative trait locus; production trait; transgenic animal; fat reduction.
XX					XX	KW
DT 26-JUN-1998 (first entry)					OS Sus scrofa.	
XX					XX	
DE Bovine myelin P2 protein.					PN WO973588-A2.	
XX					XX	
KW Bovine; myelin; P2 protein; treatment; inflammatory polyneuritis;					PD 02-OCT-1997.	
KW Guillain-Barre syndrome; vasculitis; nerve inflammation;					XX	
KW gammopathy.					PF 27-MAR-1997;	97WO-NL00157.
XX					XX	
OS Bos taurus.					PR 28-MAR-1996;	96EP-0200855.
XX					XX	
PN WO9803647-A2.					PA (DALL-) DALIAND BV.	
XX					PA (IDER-) INST DIERHOUDERIJ EN DIERGEZONDHEID ID-D.	
PD 29-JAN-1998.					PA (INNEV-) NOORD NEDERLANDS VARKENSSTAMBOEK BV.	
XX					PA (PROV-) PROVA BV.	
PF 18-JUL-1997;					PA (STAM-) STAMBOEK ZUID BV.	
XX					XX	
PR 18-JUL-1996;					PI Gerbens F;	
XX					XX	
PA (GOLD/) GOLD R.					DR WPI; 1997-489563/45.	
PA (WEISS/) WEISCHAUPT A.					XX	
XX					PT Pig heart fatty acid-binding protein gene - used to identify	
PI Gold R, Weishaupt A;					PT polymorphisms associated with production traits, e.g. body weight,	
XX					PT intramuscular fat	
DR WPI; 1998-120772/11.					XX	
PT Recombinant myelin proteins for treating T-cell mediated disease of					PS Claim 1; Fig 1; 41PP; English.	
PT peripheral nervous system - by high dose antigen therapy, causing					XX	
PT apoptosis in T cells, for treating e.g. polyneuritis or					CC The present sequence is porcine heart-fatty acid binding	
PT Guillain-Barre syndrome					CC protein (H-FABP). The H-FABP gene can be used to localise, identify	
XX					CC especially where these are associated with production traits.	
PS Disclosure: Fig 4; 14pp; German.					CC Alleles of the porcine H-FABP gene can be marked, allowing them to	
XX					CC be distinguished, preferably by detection of specific restriction	
PT sites, e.g. MspI, HaeIII or Hinfl. The H-FABP gene can also be used					CC CC or mark porcine genes, alleles or quantitative trait loci,	
PT to localise, identify or mark genes, alleles or quantitative trait					CC CC loci in samples by amplification of specific genomic fragments. By	
PT Guillain-Barre syndrome, vasculitis and nerve inflammation in cases					CC CC using samples large numbers of pigs can be genotyped rapidly. The	
CC of gammopathy.					CC methods can be used to identify differences between pig alleles	
XX					CC CC associated with improvements in production traits, and in marker	
CC assisted identification/selection of pigs. The H-FABP gene can also					CC CC be used to generate transgenic animals encoding desirable alleles	
CC of H-FABP.					CC CC of H-FABP, to enhance production or physiological characteristics.	
CC Specific allelic proteins or peptides may also be produced from the					CC CC gene. Such peptides, or antibodies directed against them, can be	
CC culture, or in diagnostic tests to select animals expressing					CC CC desired forms of allelic proteins/fragments. Fat reduction is	
CC desired forms of allelic proteins/fragments. Fat reduction is					CC CC desirable in pig breeding because of interest in lean meat, but	
CC previous efforts to reduce backfat deposits have also decreased					CC CC	
SQ Sequence 136 AA;						
QY	65.9%	Score 445;	DB 19;	Length 136;	DB 6	1 MCDAFGVGTWKLYSSENFDYYMKVEGVGPATRKVAGMAKPNMIIISVNGDVTIKSESTFKN 60
Best Local Similarity 66.2%	Pred. No. 3.3e-44;				XX	
Matches 86; Conservative 17; Mismatches 27;	Indels 0;	Gaps 0;			DB 1 msnkflgwtwklyssenfdyemkalgvlgratrkgnlakppvistespfkntirtespfknt 60	

CC intramuscular fat (IMF), important for taste. The H-FABP gene is a
 CC muscle specific candidate for the putative gene for IMF deposition
 CC in pigs. Variation in this gene is responsible for variation in
 CC IMF % and backfat thickness, and will affect other production
 CC traits, e.g. average daily weight gain and feed efficiency, since
 CC fat production and deposition is energy consuming, detracting
 CC energy from other purposes, e.g. analysis of body weight (BW) and
 CC IMF by Statistical Analysis System (SAS) statistics programme
 CC showed a significant difference in BW, and a distinct but not
 CC significant difference in IMF %.
 XX Sequence 134 AA;

Query Match 64.5%; Score 435.5; DB 18; Length 134;
 Best Local Similarity 64.4%; Pred. No. 4.2e-4;
 Matches 85; Conservative 15; Mismatches 31; Indels 1; Gaps 1;
 Oy 1 MCDAFVGTWKLVSSENNDDYMKKEVGVGFATRKVAGNAKPNNLISNGDVITIKSESTFKN 60
 Db 1 mvdafatwk1vdsknfddmksigfpatqvanntkpttiiengdtiiktstfk 60
 Qy 61 TEISFLGQEFDEVTADRKVSKTINLDGGYLHVYOKWDGKSTTIKRKREDDKLVYECVM 120
 Qy 61 TEISFLGQEFDEVTADRKVSKTINLDGGYLHVYOKWDGKSTTIKRKREDDKLVYECVM 120
 Db 61 teisflgqefdettdaddrkvsivtlggkvhlgkwngdettivrelvdygkllith 120
 Qy 121 KGVTSRHYERA 132
 ID 121 gdvavavhyeka 132
 DR 121 gsavcrctyek 132

RESULT 11.

AAW8049

standard; Protein; 132 AA.

XX

AAW8049;

AC

AAW8049;

DT

16-FEB-1999

(first entry)

XX

Amino acid sequence of the human fatty acid binding protein.

ID

AAW8049

DE

XX

Human; fatty acid binding protein; Hu-FABP; developmental disorder;

KW

cancer; spina bifida; hydrocephalus; hereditary neuropathy;

KW

Charcot-Marie-Tooth disease; neurofibromatosis; antagonist;

KW

hyperaldosteronism; adenocarcinoma.

XX

Homo sapiens.

OS

XX

WO845440-A1.

PN

XX

15-OCT-1998.

PR

XX

98WO-US07084.

AC

XX

08-APR-1998;

PR

XX

97US-0825783.

XX

(INCY) INCYTE PHARM INC.

PA

XX

Hillman JE,

PI

Shah P;

XX

WPI; 1998-594484/50.

DR

XX

N-PSDP; AAV68587.

PS

XX

New isolated human fatty acid binding protein - used to develop

PT

PT products for treating, e.g. spina bifida, anaemia, glaucoma, seizure

PT

PT disorders, epilepsy and cerebrovascular disease

XX

Claim 1; Fig 1; 59PP.

XX

English.

XX

Human cytostatin II (AAW2408) is related by amino sequence homology

CC to mammary derived growth inhibitor found in cattle and mice. Its

CC amino acid sequence was deduced from a cDNA clone (AAT7751) obt.

CC from a foetal brain library. Recombinant cytostatin II can be

CC expressed in prokaryotic or eukaryotic host cells. It can be used

CC differentiation, e.g. hyperalsteronism, and cancers including

CC to inhibit growth and differentiation of tumour cells, or venous
 CC endothelial cells to prevent, slow or alter angiogenesis. It also
 CC inhibits mammary epithelial cell growth and modulates mammary gland
 CC differentiation and may be used to aid milk production in human
 CC mothers or to modulate breast size e.g. after parturition.
 XX Sequence 132 AA;

SQ

Query Match 59.1%; Score 399; DB 18;

Best Local Similarity 56.8%; Pred. No. 7.6e-39;

Matches 21; Mismatches 36; Indels 0; Gaps 0;

Oy 1 MCDAFVGTWKLVSSENNDDYMKKEVGVGFATRKVAGNAKPNNLISNGDVITIKSESTFKN 60

Db 1 mveafcatwk1ltnsnqnfrdeynkalgvgftrqgvnvtkpviisegdkvvirtstfk 60

Qy 61 TEISFLGQEFDEVTADRKVSKTINLDGGYLHVYOKWDGKSTTIKRKREDDKLVYECVM 120

Db 61 teisflgqefdettdaddrcksvsldgdkvhlgkwngdettivrekdgkmvmtltf 120

Qy 121 KGVTSRHYERA 132

Db 121 gdvavavhyeka 132

RESULT 11.

AAW8049

ID AAW8049 standard; Protein; 132 AA.

XX

AAW8049;

AC

AAW8049;

DT

16-FEB-1999

(first entry)

XX

Amino acid sequence of the human fatty acid binding protein.

ID

AAW8049

DE

XX

Human; fatty acid binding protein; Hu-FABP; developmental disorder;

KW

cancer; spina bifida; hydrocephalus; hereditary neuropathy;

KW

Charcot-Marie-Tooth disease; neurofibromatosis; antagonist;

KW

hyperaldosteronism; adenocarcinoma.

XX

Homo sapiens.

OS

XX

WO845440-A1.

PN

XX

15-OCT-1998.

PR

XX

98WO-US07084.

AC

XX

08-APR-1998;

PR

XX

97US-0825783.

XX

(INCY) INCYTE PHARM INC.

PA

XX

Hillman JE,

PI

Shah P;

XX

WPI; 1998-594484/50.

DR

XX

N-PSDP; AAV68587.

PS

XX

New isolated human fatty acid binding protein - used to develop

PT

PT products for treating, e.g. spina bifida, anaemia, seizure

PT

PT disorders, epilepsy and cerebrovascular disease

XX

Claim 1; Fig 1; 59PP.

XX

English.

XX

Human cytostatin II (AAW2408) is related by amino sequence homology

CC to mammary derived growth inhibitor found in cattle and mice. Its

CC amino acid sequence was deduced from a cDNA clone (AAT7751) obt.

CC from a foetal brain library. Recombinant cytostatin II can be

CC expressed in prokaryotic or eukaryotic host cells. It can be used

CC differentiation, e.g. hyperalsteronism, and cancers including

CC

RESULT 14
AAG0347 Human secreted protein, SEQ ID NO: 7928.
D AAG03847 standard; Protein: 117 AA.
X X X X Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
X X X X gene therapy; chromosome mapping.
AC AAG03847;
CX CX 06-OCT-2000 (first entry)

N-PSDB; AAC03835.

New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures -

Claim 13: SEQ ID 7928; 71pp + CD-ROM; English.

The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or poly+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from Oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.

sq	Sequence	117 AA;	Query Match	58.7%	Score	396;	DB	21;	Length	117;
dy			Best Local Similarity	69.1%	Pred. No.	1.4e-38;				
dy			Matches	76;	Mismatches	13;	Indels	0;	Gaps	
dy			Conservative	13;						
db										
dy			1	MCDAFGTWKLVSSSENEDDMKEYGVGFATRKVAGMAKENPMILSVNGDVITIKSESEFKN	60					
dy				: :						
dy			1	msnkltgtwlkvssnenfdymkaigqlatrkglnapktvilskkgditlirtestfkn	60					
dy			61	TEISPLFGQEQDETAADDRKVKSTTLDGGVLVHEVQKDGKSKTTIKRRE	110					

Db 61 telisfkligqefeteetadnrktsivtliqrgslninqvrdgkettikrase 110
 RESULT 15
 AAC66580 AAC66580 standard; Protein; 131 AA.
 ID XX
 AC AAC66580.
 NNNNNNNNNN.

DT	22-OCT-2001	(first entry)
XX	Human cytostatin II polypeptide.	
DE		
XX		
KW	Human; cytostatin III; cytostatic; epithelial cell growth;	
KW	milk production; breast involution; cardiac myocyte hypertrophy;	
KW	leukaemia; cytostatin II.	
XX		
OS	Homo sapiens.	
XX		
PN	US6232291-B1.	
XX		
PD	15-MAY-2001.	

XX	PF	10-MAY-1999;	99US-0307817.
XX	PR	19-MAR-1996;	96US-0013655.
XX	PR	19-MAR-1997;	97US-0820825.
PA	(HUMA -) HUMAN GENOME SCI INC.		
XX	PI	Ni J, Yu G, Gentz R, Dillon PJ;	
XX	DR	WPI; 2001-342775/36.	
XX	PT	Cytostatin III polypeptides that modulate growth of epithelial cells,	
XX	PT	stimulate milk production in humans and cows and promote involution of	
XX	PT	breast, for research, biological, clinical and therapeutic purposes -	

PS Disclosure; Fig 2; 31pp; English.
 XX
 CC The invention relates to an isolated Cytostatin III polypeptide,
 CC comprising a sequence selected from amino acids 1-35, 2-135, 108-135,
 CC 119-135 and 118-125, of a sequence of 135 amino acids fully defined in
 CC the specification. The polypeptide is useful for modulating growth of
 CC epithelial cells, for stimulating milk production in humans and cows,
 CC and for promoting involution of breasts. It is also useful for research,
 CC cardiac myocyte hypertrophy and leukaemia, and is useful for research,
 CC and biological, clinical and therapeutic purposes. The present
 CC sequence is provided in the specification for research purposes
 CC with human cytostatin III.
 XX Sequence 131 AA;
 SQ Score 386.5; DB 22; Length 131;
 Query Match 57.3%; Best Local Similarity 56.8%; Pred. No. 2; e-37;
 Best Local Similarity 56.8%; Pred. No. 2; e-37;
 Matches 75; Conservative 20; Mismatches 36; Indels 1; Gaps 0
 QY 1 MCDAFVGFTWKLVSSENFDYYMKEYGVGFATRKVAGAKPNMTISVNGDVITKSESTEKN 60

Db	1	mveafcatwltnsnfdeymkalgvfatrqvgnutkptvlisqeqdvvirtlstfk	60
Qy	61	TEISFILGQEFDETYADDRKVSKTSTLTDGGVYQKWDGKSTTIIKRREDDKKLYVECM	120
Db	61	telfsfqg-efdettdaddrcksrvslldgdkvhilqwdgktnfreikdgkmvmtlf	119
Qy	121	KGYTSTRVYERA	132
Db	120	gdvvavryeka	131

Search completed: January 24, 2002, 09:15:21

Thu Jan 24 09:20:13 2002

us-09-905-235-1.rag

Page 9

Job time: 428 sec

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GenCore version 4.5

OM protein - protein search, using sw model

Run on: January 24, 2002, 09:09:18 ; Search time 12.53 Seconds
 (237.066 Million cell updates/sec)

Title: US-09-905-235-1

Perfect score: 675

Sequence: 1 MCDAFYGTVKLYSSENFDY KLVVECYMKGYTSTRYERA 132

Scoring table: BL0SUM62

Gapext: 0.5

Searched: 21252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 21252

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%, Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:^{*}

1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:
 2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:
 3: /cgn2_6/ptodata/2/1aa/6A_COMB.pep:
 4: /cgn2_6/ptodata/2/1aa/6B_COMB.pep:
 5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:
 6: /cgn2_6/ptodata/2/1aa/backfile1.pep:
 *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	466	69.0	131	1	US-09-409-731A-7	Sequence 7, Appli
2	466	69.0	131	2	US-08-470-298B-7	Sequence 7, Appli
3	466	69.0	133	2	US-08-820-925-11	Sequence 11, Appli
4	466	69.0	133	2	US-09-023-073A-7	Sequence 7, Appli
5	466	69.0	133	4	US-09-307-817-11	Sequence 11, Appli
6	466	69.0	133	4	US-09-361-137-7	Sequence 7, Appli
7	463	68.6	132	1	US-08-409-731A-11	Sequence 11, Appli
8	463	68.6	132	2	US-08-470-298B-11	Sequence 11, Appli
9	463	68.6	132	2	US-09-023-073A-11	Sequence 11, Appli
10	463	68.6	132	4	US-09-361-737-11	Sequence 11, Appli
11	449	66.5	133	1	US-08-409-731A-10	Sequence 10, Appli
12	449	66.5	133	2	US-08-470-298B-10	Sequence 10, Appli
13	449	66.5	133	2	US-08-820-825-13	Sequence 13, Appli
14	449	66.5	133	2	US-09-023-073A-10	Sequence 10, Appli
15	449	66.5	133	4	US-09-307-817-13	Sequence 13, Appli
16	449	66.5	133	4	US-09-361-737-10	Sequence 10, Appli
17	446	66.1	133	2	US-08-820-825-12	Sequence 12, Appli
18	446	66.1	133	4	US-09-307-817-12	Sequence 12, Appli
19	420	62.2	132	2	US-08-470-298B-12	Sequence 12, Appli
20	386.5	57.3	131	2	US-08-820-825-15	Sequence 15, Appli
21	386.5	57.3	131	4	US-09-307-817-15	Sequence 15, Appli
22	366	54.2	135	1	US-08-446-600A-4	Sequence 4, Appli
23	237	35.1	134	2	US-08-847-724-1	Sequence 1, Appli
24	229.5	34.0	133	1	US-08-554-463-1	Sequence 1, Appli
25	225	33.3	134	2	US-08-847-724-5	Sequence 5, Appli
26	225	33.3	134	2	US-09-023-073A-9	Sequence 9, Appli
27	225	33.3	134	4	US-09-361-737-9	Sequence 9, Appli

Query Match 69.0%; Score 466; DB 1; Length 131;
 Best Local Similarity 67.9%; Pred. No. 5.3e-49;
 Matches 89; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

Qy 1 MCDAFYGTVKLYSSENFDYREVGVGFTRKVAGMAPNMITSYNGCDVITIKSESTFKN 60

Db 1 MADAFVGTVKLVLDSSKNFDDYMKSLQVGFATRQVASMTKPTTIEKNGDTITKTQSTIFKN 60
 QY 61 TEISFLGQEFDETTADDRKVKSITLQDGVLVHVKNDGKSTIKRKREDDDKLUVCEVM 120
 ||::||:|||:|||:|||:|||:|||:|||:|||:|||:|||:
 Db 61 TEINFQLGTEFDETTADDRKVKSITLQDGVLVHVKNDGKSTIKRKREDDDKLUVCEVM 120
 ||::||:|||:|||:|||:|||:|||:|||:|||:|||:
 QY 121 KGVTSTRYER 131
 Db 121 GSVYSTRYER 131
 ||::||:|||:
 QY 121 KGVTSTRYER 131
 ||::||:|||:
 Db 121 GSVYSTRYER 131

RESULT 2
 US-08-470-298B-7
 ; Sequence 7, Application US/08470298B
 ; Patent No. 5844081
 ; GENERAL INFORMATION:
 ; APPLICANT: NI, JIAN
 ; APPLICANT: GENTZ, REINER L.
 ; APPLICANT: YU, GUO-LIANG
 ; APPLICANT: DILLON, PATRICK
 ; TITLE OF INVENTION: CYTOSTATIN III
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
 ; STREET: 9410 KEY WEST AVENUE
 ; CITY: ROCKVILLE
 ; STATE: MD
 ; COUNTRY: USA
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/820-825
 ; FILING DATE: 19-MAR-1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BROOKES, ANDERS A.
 ; REGISTRATION NUMBER: 36,373
 ; REFERENCE/DOCKET NUMBER: PF222
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 309-8504
 ; TELEFAX: (301) 309-8512
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 133 amino acids
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BROOKES, ALLAN A.
 ; REGISTRATION NUMBER: 36,373
 ; REFERENCE/DOCKET NUMBER: PF175D1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 301-309-8504
 ; TELEFAX: 301-309-8512
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 131 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; ORIGINAL SOURCE:
 ; ORGANISM: MDG1 (FIGURE 2)
 ; US-08-470-298B-7

Query Match 69 0%; Score 466; DB 2; Length 133;
 Best Local Similarity 67.9%; Pred. No. 5.3e-49;
 Matches 89; Conservative 15; Mismatches 27; Indels 0; Gaps 0;
 Db 1 MADAFVGTVKLVLDSSKNFDDYMKSLQVGFATRQVASMTKPTTIEKNGDTITKTQSTIFKN 60
 ||::||:|||:|||:|||:|||:|||:|||:|||:
 Db 1 MADAFVGTVKLVDSKNFDDYMKSLQVGFATRQVASMTKPTTIEKNGDTITKTQSTIFKN 60
 ||::||:|||:|||:|||:|||:|||:|||:
 QY 61 TEISFLGQEFDETTADDRKVKSITLQDGVLVHVKNDGKSTIKRKREDDDKLUVCEVM 120
 ||::||:|||:|||:|||:|||:|||:|||:
 Db 61 TEINFQLGTEFDETTADDRKVKSITLQDGVLVHVKNDGKSTIKRKREDDDKLUVCEVM 120
 ||::||:|||:|||:|||:|||:|||:
 QY 121 KGVTSTRYER 131
 ||::||:|||:
 Db 121 GSVYSTRYER 131

RESULT 3
 US-08-820-825-11
 ; Sequence 11, Application US/08820825
 ; Patent No. 5945309
 ; GENERAL INFORMATION:
 ; APPLICANT: NI, JIAN
 ; APPLICANT: YU, GUO-LIANG
 ; APPLICANT: DILLON, PATRICK
 ; TITLE OF INVENTION: CYTOSTATIN III
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
 ; STREET: 9410 KEY WEST AVENUE
 ; CITY: ROCKVILLE
 ; STATE: MD
 ; COUNTRY: USA
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/820-825
 ; FILING DATE: 19-MAR-1997
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BROOKES, ANDERS A.
 ; REGISTRATION NUMBER: 36,373
 ; REFERENCE/DOCKET NUMBER: PF222
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (301) 309-8504
 ; TELEFAX: (301) 309-8512
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 133 amino acids
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: BROOKES, ALLAN A.
 ; REGISTRATION NUMBER: 36,373
 ; REFERENCE/DOCKET NUMBER: PF175D1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 301-309-8504
 ; TELEFAX: 301-309-8512
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 131 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; ORIGINAL SOURCE:
 ; ORGANISM: MDG1 (FIGURE 2)
 ; US-08-820-825-11

Query Match 69 0%; Score 466; DB 2; Length 133;
 Best Local Similarity 67.9%; Pred. No. 5.3e-49;
 Matches 89; Conservative 15; Mismatches 27; Indels 0; Gaps 0;
 Db 121 GSVYSTRYER 131
 ; Sequence 7, Application US/09023073A
 ; Patent No. 5977309
 ; GENERAL INFORMATION:
 ; APPLICANT: NI, JIAN
 ; APPLICANT: GENTZ, Reiner L.
 ; APPLICANT: YU, Guo-Liang
 ; APPLICANT: ROSEN, Craig A.
 ; TITLE OF INVENTION: Cytostatin I
 ; NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:
 ADDRESSEE: HUMAN GENOME SCIENCES, INC.
 STREET: 9410 KEY WEST AVENUE
 CITY: ROCKVILLE
 STATE: MARYLAND
 COUNTRY: USA
 ZIP: 20850

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0,
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/023, 073A
 FILING DATE: 13-FEB-1998
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: Wales, Michele M.
 REGISTRATION NUMBER: P-43-975
 REFERENCE/DOCKET NUMBER: PF175D
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 301-610-5772
 TELEFAX: 301-309-8439
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 133 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-023-073A-7

Query Match 69.0%; Score 466; DB 2; Length 133;

Best Local Similarity 67.9%; Pred. No. 5, 4e-49;
 Matches 89; Conservative 15; Indels 0; Gaps 0;

QY 1 MCDAFVGTVKLVSSENDDYMKKEYGVGFRTRKVAGMAKPNNMISVNGDVITIKSESTPKN 60
 DB 1 MADAFVGTVKLVDSKNFDDYMKSGVGPATRQASMTKPTTIEKNGDTITKTQSTPKN 60

QY 61 TEISFILGOEFDDEVTAADRKVKSTTLDGGVLYHQKNDGKSTTIRKREDDKLVVECYM 120
 DB 61 TEINFGQLEFDEVTAADRKVKSLVTDGGKLTHVORKNGOETTLRELVGKLILTH 120

QY 121 KGVTSTRYER 131
 DB 121 GSVVSTRYEK 131

RESULT 5
 US-09-307-817-11
 Sequence 11, Application US/09307817
 Patent No. 6232291
 GENERAL INFORMATION:
 APPLICANT: NI, JIAN
 APPLICANT: YU, GUO-LIANG
 APPLICANT: GENTZ, REINER L.
 APPLICANT: DILLON, PATRICK
 TITLE OF INVENTION: CYTOSTATIN III
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HUMAN GENOME SCIENCES, INC.
 STREET: 9410 KEY WEST AVENUE
 CITY: ROCKVILLE
 STATE: MD
 COUNTRY: USA
 ZIP: 20850

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/361,737
 FILING DATE: 13-FEB-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Wales, Michele M.

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/307, 817
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/820, 825
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: BROOKES, ANDERS A.
 REGISTRATION NUMBER: 36, 373
 REFERENCE/DOCKET NUMBER: PF222
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 309-9504
 TELEFAX: (301) 309-8512
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 133 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-307-817-11

Query Match 69.0%; Score 466; DB 4; Length 133;
 Best Local Similarity 67.9%; Pred. No. 5, 4e-49;
 Matches 89; Conservative 15; Indels 0; Gaps 0;

QY 1 MCDAFVGTVKLVSSENDDYMKKEYGVGFRTRKVAGMAKPNNMISVNGDVITIKSESTPKN 60
 DB 1 MADAFVGTVKLVDSKNFDDYMKSGVGPATRQASMTKPTTIEKNGDTITKTQSTPKN 60

RESULT 6
 US-09-361-737-7
 Sequence 7, Application US/09361737
 Patent No. 6287812
 GENERAL INFORMATION:
 APPLICANT: NI, JIAN
 APPLICANT: GENTZ, REINER
 APPLICANT: YU, GUO-LIANG
 APPLICANT: ROSEN, CRAIG A
 TITLE OF INVENTION: Cytostatin I
 NUMBER OF SEQUENCES: 11
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HUMAN GENOME SCIENCES, INC.
 STREET: 9410 KEY WEST AVENUE
 CITY: ROCKVILLE
 STATE: MARYLAND
 COUNTY: USA
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/361,737
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: Wales, Michele M.

REGISTRATION NUMBER: P-43,975
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 301-610-5772
 TELEFAX: 301-309-8439
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 133 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-09-361-737-7

Query Match 69.0%; Score 466; DB 4; Length 133;
 Best Local Similarity 67.9%; Pred. No. 5.4e-49;
 Matches 89; Conservative 15; Mismatches 27; Indels 0; Gaps 0;

Qy 1 MCDAFVGWKLVSSENFDYMKEVGFGPATRKVAGMAKPNNMISVNGDVITKSESTPKN 60

Db 1 MADAFVGWKLVDSKNFDYMKEVGFGPATRKVAGMAKPNNMISVNGDVITKSESTPKN 60

Qy 61 TEISFILGQEFDDEVADDRKVSKTILDGGVLYHVQWDGKSTIKRKEDDKLVYECVM 120

Db 61 TEINFQLGTEFDEVADDRKVSKLVLTDGGKLVHVKWNGQETTLRELVGKLILTH 120

Qy. 121 KGVTSTRYER 131

Db 121 GSIVSTRYER 131

RESULT 7
 Sequence 11, Application US/08409731A
 Patent No. 5658758

GENERAL INFORMATION:

APPLICANT: Yu, Guo-Liang
 APPLICANT: Genz, Reiner

APPLICANT: Rosen, Craig A.
 TITLE OF INVENTION: CYTOSTATIN I

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: HUMAN GENOME SCIENCES, INC.

STREET: 9410 KEY WEST AVENUE
 CITY: ROCKVILLE
 STATE: MD
 COUNTRY: USA
 ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/409731A

FILING DATE: 24-MAR-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Benson, Robert H.

REGISTRATION NUMBER: 30,446

REFERENCE/DOCKET NUMBER: PF175

TELECOMMUNICATION INFORMATION:

TELEFAX: 301-309-8504

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 132 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE: ORGANISM: MYELIN P2 (FIGURE 2)

RESULT 8
 Sequence 11, Application US/08470298B

Patent No. 5844081

GENERAL INFORMATION:

APPLICANT: Ni, Jian

APPLICANT: GENTZ, Reiner

APPLICANT: Yu, Guo-Liang

APPLICANT: ROSEN, CRAIG A.

TITLE OF INVENTION: CYTOSTATIN I

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: HUMAN GENOME SCIENCES, INC.

STREET: 9410 KEY WEST AVENUE

CITY: ROCKVILLE

STATE: MD

COUNTRY: US

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/470298B

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: BROOKES, ALLAN A.

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PF175D1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-309-8504

TELEFAX: 301-309-8512

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 132 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE: ORGANISM: MYELIN P2 (FIGURE 2)

RESULT 9
 Sequence 11, Application US/08-409-731A-11

Patent No. 5658758

GENERAL INFORMATION:

APPLICANT: Ni, Jian

APPLICANT: Genz, Reiner

APPLICANT: Rosen, Craig A.

TITLE OF INVENTION: CYTOSTATIN I

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: HUMAN GENOME SCIENCES, INC.

STREET: 9410 KEY WEST AVENUE

CITY: ROCKVILLE

STATE: MD

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/409731A

FILING DATE: 24-MAR-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Benson, Robert H.

REGISTRATION NUMBER: 30,446

REFERENCE/DOCKET NUMBER: PF175

TELECOMMUNICATION INFORMATION:

TELEFAX: 301-309-8504

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 132 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE: ORGANISM: MYELIN P2 (FIGURE 2)

Query Match 68.6%; Score 463; DB 1; Length 132;

Best Local Similarity 67.2%; Pred. No. 1.2e-48;

Matches 88; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

Qy 1 MCDAFVGWKLVSSENFDYMKEVGFGPATRKVAGMAKPNNMISVNGDVITKSESTPKN 60

Db 1 MSNFKLGTVLSSENFDYMKALGVGLATRKGNLAPTPVILSKKGDDITIRTESTPKN 60

Qy 61 TEISFILGQEFDDEVADDRKVSKTILDGGVLYHVQWDGKSTIKRKEDDKLVYECVM 120

Db 61 TEISFILGQEFDDEVADDRKVSKLVLTDGGKLVHVKWNGQETTLRELVGKLILTH 120

Qy. 121 KGVTSTRYER 131

Db 121 GSIVSTRYER 131

RESULT 8
 Sequence 11, Application US/08470298B

Patent No. 5844081

GENERAL INFORMATION:

APPLICANT: Ni, Jian

APPLICANT: GENTZ, Reiner

APPLICANT: Yu, Guo-Liang

APPLICANT: ROSEN, CRAIG A.

TITLE OF INVENTION: CYTOSTATIN I

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: HUMAN GENOME SCIENCES, INC.

STREET: 9410 KEY WEST AVENUE

CITY: ROCKVILLE

STATE: MD

COUNTRY: US

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/470298B

FILING DATE: 06-JUN-1995

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: BROOKES, ALLAN A.

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PF175D1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-309-8504

TELEFAX: 301-309-8512

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 132 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

ORIGINAL SOURCE: ORGANISM: MYELIN P2 (FIGURE 2)

US-08-470-298B-11

Query Match 68.6%; Score 463; DB 2; Length 132;

Best Local Similarity 67.2%; Pred. No. 1.2e-48;

Matches 88; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

Qy 1 MCDAFVGWKLVSSENFDYMKEVGFGPATRKVAGMAKPNNMISVNGDVITKSESTPKN 60

Db 1 MSNFKLGTVLSSENFDYMKALGVGLATRKGNLAPTPVILSKKGDDITIRTESTPKN 60

RESULT 9
 QY 61 TEISFILGQEFDEVADDRKVKSTITLDGVLYHVQKDGSSTIKRKEDDKLVVECM 120
 ; Sequence 11, Application US/09361737
 ; Patent No. 6287812
 ; GENERAL INFORMATION:
 ; APPLICANT: Ni, Jian
 ; APPLICANT: Genthz, Reiner
 ; APPLICANT: Yu, Guo-Liang
 ; APPLICANT: Rosen, Craig A.
 ; TITLE OF INVENTION: Cystostatin I
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
 ; STREET: 9410 KEY WEST AVENUE
 ; CITY: ROCKVILLE
 ; STATE: MARYLAND
 ; COUNTRY: USA
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/361,737
 ; FILING DATE:
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 09/023,073
 ; FILING DATE: 13-FEB-1998
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Wales, Michele M.
 ; REGISTRATION NUMBER: P-43,975
 ; REFERENCE/DOCKET NUMBER: PF175D2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 301-610-5772
 ; TELEFAX: 301-309-8439
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 132 amino acids
 ; STRANDEDNESS: single
 ; TOPOLOGY: Linear
 ; MOLECULE TYPE: protein
 ; US-09-361-737-11

Query Match 68.6%; Score 463; DB 4; Length 132;
 Best Local Similarity 67.2%; Pred. No. 1.2e-48;
 Matches 88; Conservative 17; N mismatches 26; Indels 0; Gaps 0;
 ; GENERAL INFORMATION:
 ; APPLICANT: Ni, Jian
 ; APPLICANT: Genthz, Reiner
 ; APPLICANT: Yu, Guo-Liang
 ; APPLICANT: Rosen, Craig A.
 ; TITLE OF INVENTION: Cystostatin I
 ; NUMBER OF SEQUENCES: 11

QY 61 TEISFILGQEFDEVADDRKVKSTITLDGVLYHVQKDGSSTIKRKEDDKLVVECM 120
 ; Sequence 11, Application US/09023073A
 ; Patent No. 5977309
 ; GENERAL INFORMATION:
 ; APPLICANT: Ni, Jian
 ; APPLICANT: Genthz, Reiner
 ; APPLICANT: Yu, Guo-Liang
 ; APPLICANT: Rosen, Craig A.
 ; TITLE OF INVENTION: Cystostatin I
 ; NUMBER OF SEQUENCES: 11
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
 ; STREET: 9410 KEY WEST AVENUE
 ; CITY: ROCKVILLE
 ; STATE: MARYLAND
 ; COUNTRY: USA
 ; ZIP: 20850
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; APPLICATION NUMBER: US/09/023,073A
 ; FILING DATE: 13-FEB-1998
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Wales, Michele M.
 ; REGISTRATION NUMBER: P-43,975
 ; REFERENCE/DOCKET NUMBER: PF175D2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 301-610-5772
 ; TELEFAX: 301-309-8439
 ; INFORMATION FOR SEQ ID NO: 11:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 132 amino acids
 ; STRANDEDNESS: single
 ; TOPOLOGY: Linear
 ; MOLECULE TYPE: protein
 ; US-09-023-073A-11

Query Match 68.6%; Score 463; DB 4; Length 132;
 Best Local Similarity 67.2%; Pred. No. 1.2e-48;
 Matches 88; Conservative 17; N mismatches 26; Indels 0; Gaps 0;
 ; GENERAL INFORMATION:
 ; APPLICANT: Ni, Jian
 ; APPLICANT: Genthz, Reiner
 ; APPLICANT: Yu, Guo-Liang
 ; APPLICANT: Rosen, Craig A.
 ; TITLE OF INVENTION: Cystostatin I
 ; NUMBER OF SEQUENCES: 11

QY 1 MCDAFVGTVWKLVSENFDDYMKVKEVGVGPATRYAGMAKPNNMISVNGDVITKSESTFKN 60
 ; Sequence 10, Application US/08409731A
 ; Patent No. 5658758
 ; GENERAL INFORMATION:
 ; APPLICANT: Ni, Jian
 ; APPLICANT: Genthz, Reiner
 ; APPLICANT: Yu, Guo-Liang
 ; APPLICANT: Rosen, Craig A.
 ; TITLE OF INVENTION: Cystostatin I
 ; NUMBER OF SEQUENCES: 11

Query Match 68.6%; Score 463; DB 2; Length 132;
 Best Local Similarity 67.2%; Pred. No. 1.2e-48;
 Matches 88; Conservative 17; N mismatches 26; Indels 0; Gaps 0;
 ; GENERAL INFORMATION:
 ; APPLICANT: Ni, Jian
 ; APPLICANT: Genthz, Reiner
 ; APPLICANT: Yu, Guo-Liang
 ; APPLICANT: Rosen, Craig A.
 ; TITLE OF INVENTION: Cystostatin I
 ; NUMBER OF SEQUENCES: 11

Query Match 68.6%; Score 463; DB 2; Length 132;
 Best Local Similarity 67.2%; Pred. No. 1.2e-48;
 Matches 88; Conservative 17; N mismatches 26; Indels 0; Gaps 0;
 ; GENERAL INFORMATION:
 ; APPLICANT: Ni, Jian
 ; APPLICANT: Genthz, Reiner
 ; APPLICANT: Yu, Guo-Liang
 ; APPLICANT: Rosen, Craig A.
 ; TITLE OF INVENTION: Cystostatin I
 ; NUMBER OF SEQUENCES: 11

Query Match 68.6%; Score 463; DB 4; Length 132;
 Best Local Similarity 67.2%; Pred. No. 1.2e-48;
 Matches 88; Conservative 17; N mismatches 26; Indels 0; Gaps 0;
 ; GENERAL INFORMATION:
 ; APPLICANT: Ni, Jian
 ; APPLICANT: Genthz, Reiner
 ; APPLICANT: Yu, Guo-Liang
 ; APPLICANT: Rosen, Craig A.
 ; TITLE OF INVENTION: Cystostatin I
 ; NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:
 ADDRESSEE: HUMAN GENOME SCIENCES, INC.
 STREET: 9410 KEY WEST AVENUE
 CITY: ROCKVILLE
 STATE: MD
 COUNTRY: USA
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: FLOPPY disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US-08/409,731A
 FILING DATE: 24-MAR-1995
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Benson, Robert H.
 REGISTRATION NUMBER: 30,446
 REFERENCE DOCKET NUMBER: PF175
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 301-309-8504
 TELEFAX: 301-309-8512
 INFORMATION FOR SEQ ID NO: 10:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 133 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-409-731A-10

Query Match 66.5%; Score 449; DB 1; Length 133;
 Best Local Similarity 64.9%; Pred. No. 6.3e-4;
 Matches 85; Conservative 16; Mismatches 30; Indels 0; Gaps 0;

Qy 1 MCDAFWGTWKLYSSENEDYMEKVGVGFATRKVAGMAKPNMISVNGDVITIKSESTFKN 60
 Db 1 MVDAGLFTWKLYDSKNEFDYMKSLGVTGFAVQASWTKPTTIEKGDLTILKTHSTFKN 60

Qy 61 TEISFILQEFDETTADDRKVKSIVTLDGGKLVHLQRWDQETTLVRELIDGKLILTH 120
 Db 61 TEISFKLGVFDETTADDRKVKSIVTLDGGKLVHLQRWDQETTLVRELIDGKLILTH 120

RESULT 13
 US-08-820-825-13
 Sequence 13, Application US/08820825
 Patent No. 5945309
 GENERAL INFORMATION:
 APPLICANT: NI, JIAN
 APPLICANT: YU, GUO-LIANG
 APPLICANT: GENTZ, REINER L.
 APPLICANT: DILLON, PATRICK
 TITLE OF INVENTION: CYTOSTATIN III
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HUMAN GENOME SCIENCES, INC.
 STREET: 9410 KEY WEST AVENUE
 CITY: ROCKVILLE
 STATE: MD
 COUNTRY: USA
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

RESULT 12
 US-08-470-238B-10
 Sequence 10, Application US/08470238B
 Patent No. 5844081
 GENERAL INFORMATION:
 APPLICANT: NI, JIAN
 APPLICANT: GENTZ, REINER
 APPLICANT: YU, GUO-LIANG
 APPLICANT: ROSEN, CRAIG A.
 TITLE OF INVENTION: CYTOSTATIN I
 NUMBER OF SEQUENCES: 12
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: HUMAN GENOME SCIENCES, INC.
 STREET: 9410 KEY WEST AVENUE
 CITY: ROCKVILLE
 STATE: MD
 COUNTRY: US
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30

Db 61 TEISFKLGVEFIDETADDRKVKSIVTLDDGGKLVHLQRWDGQIETTLVREBLIDGKLILTLTH 1.20
Qy 121 KGTMSTRYER 131
| | | :
Db 121 GTAVCTRTYEK 131

Search completed: January 24, 2002, 09:15:40
Job time: 382 sec

Db 1 MCDAFVGTVKLVSSENDDYMEKEYGVGFATRKVAGMAKPNNMIIISVNGDVTIKSESTFKN 60
 Qy 61 TEISFILQEEFDEVADDRKVKSITLDDGVLVHVKWDGKSTTIKRREDDKLVVECM 120
 Db 61 TEISFILQEEFDEVADDRKVKSITLDDGVLVHVKWDGKSTTIKRREDDKLVVECM 120
 Qy 121 KGVTSTRYERA 132
 Db 121 KGVTSTRYERA 132

RESULT 2
 US-09-391-053A-1
 ; Sequence 1, Application US/09391053A
 ; GENERAL INFORMATION:
 ; APPLICANT: BRISTOL-MYERS SQUIBB COMPANY
 ; TITLE OF INVENTION: METHOD FOR TREATING DIABETES EMPLOYING AN AP2 INHIBITOR AND CO
 ; FILE REFERENCE: LA24a
 ; CURRENT APPLICATION NUMBER: US/09/905,235
 ; CURRENT FILING DATE: 2001-07-13
 ; NUMBER OF SEQ ID NOS: 1
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 1
 ; LENGTH: 132
 ; TYPE: PRT
 ; ORGANISM: HOMO SAPIENS
 US-09-391-053A-1

Query Match 100.0%; Score 675; DB 17; Length 132;
 Best Local Similarity 100.0%; Pred. No. 2.1e-67;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCDAFVGTVKLVSSENDDYMEKEYGVGFATRKVAGMAKPNNMIIISVNGDVTIKSESTFKN 60
 Db 1 MCDAFVGTVKLVSSENDDYMEKEYGVGFATRKVAGMAKPNNMIIISVNGDVTIKSESTFKN 60
 Qy 61 TEISFILQEEFDEVADDRKVKSITLDDGVLVHVKWDGKSTTIKRREDDKLVVECM 120
 Db 61 TEISFILQEEFDEVADDRKVKSITLDDGVLVHVKWDGKSTTIKRREDDKLVVECM 120
 Qy 121 KGVTSTRYERA 132
 Db 121 KGVTSTRYERA 132

RESULT 4
 US-09-905-235-1
 ; Sequence 1, Application US/0905235
 ; GENERAL INFORMATION:
 ; APPLICANT: BRISTOL-MYERS SQUIBB COMPANY
 ; TITLE OF INVENTION: METHOD FOR TREATING DIABETES EMPLOYING AN AP2 INHIBITOR AND CO
 ; FILE REFERENCE: LA24a
 ; CURRENT APPLICATION NUMBER: US/09/905,235
 ; CURRENT FILING DATE: 2001-07-13
 ; NUMBER OF SEQ ID NOS: 1
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO: 1
 ; LENGTH: 132
 ; TYPE: PRT
 ; ORGANISM: HOMO SAPIENS
 US-09-905-235-1

Query Match 100.0%; Score 675; DB 23; Length 132;
 Best Local Similarity 100.0%; Pred. No. 2.1e-67;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCDAFVGTVKLVSSENDDYMEKEYGVGFATRKVAGMAKPNNMIIISVNGDVTIKSESTFKN 60
 Db 1 MCDAFVGTVKLVSSENDDYMEKEYGVGFATRKVAGMAKPNNMIIISVNGDVTIKSESTFKN 60
 Qy 61 TEISFILQEEFDEVADDRKVKSITLDDGVLVHVKWDGKSTTIKRREDDKLVVECM 120
 Db 61 TEISFILQEEFDEVADDRKVKSITLDDGVLVHVKWDGKSTTIKRREDDKLVVECM 120
 Qy 121 KGVTSTRYERA 132
 Db 121 KGVTSTRYERA 132

RESULT 5
 US-09-760-469-913
 ; Sequence 913, Application US/09760469
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PtZ54
 ; CURRENT APPLICATION NUMBER: US/09/760,469
 ; CURRENT FILING DATE: 2001-01-16
 ; Prior application data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 1983
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 913
 ; LENGTH: 136
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-760-469-913

Query Match 100.0%; Score 675; DB 21; Length 136;
 Best Local Similarity 100.0%; Pred. No. 2.2e-67;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCDAFVGTVKLVSSENDDYMEKEYGVGFATRKVAGMAKPNNMIIISVNGDVTIKSESTFKN 60
 Db 5 MCDAFVGTVKLVSSENDDYMEKEYGVGFATRKVAGMAKPNNMIIISVNGDVTIKSESTFKN 64
 Qy 61 TEISFILQEEFDEVADDRKVKSITLDDGVLVHVKWDGKSTTIKRREDDKLVVECM 120

Db 65 TEISFILGQEFDEVTADRKVKSTITLDGGVLYHVQKWDGKSTTIKRKREDDKLVVECM 124
 Qy 121 KGVTSTRYERA 132
 Db 125 KGVTSTRYERA 136

RESULT 6
 US-09-760-469-915
 ; Sequence 915, Application US/09760469
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PTZ54
 ; CURRENT APPLICATION NUMBER: US/09/760,469
 ; CURRENT FILING DATE: 2001-01-16
 ; PRIOR APPLICATION data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 1983
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 915
 ; LENGTH: 136
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-760-469-915

Query Match 100.0%; Score 675; DB 21; Length 136;
 Best Local Similarity 100.0%; Pred. No. 2.2e-67;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCDAFVGWKLVSSENFDYMKVEGVGFATRKVAGMAKPNMIIISVNGDVTIKSESTFKN 60
 Db 5 MCDAFVGWKLVSSENFDYMKVEGVGFATRKVAGMAKPNMIIISVNGDVTIKSESTFKN 64
 Qy 61 TEISFILGQEFDEVTADRKVKSTITLDGGVLYHVQKWDGKSTTIKRKREDDKLVVECM 120
 Db 65 TEISFILGQEFDEVTADRKVKSTITLDGGVLYHVQKWDGKSTTIKRKREDDKLVVECM 124
 Qy 121 KGVTSTRYERA 132
 Db 125 KGVTSTRYERA 136

RESULT 7
 US-09-760-469-917
 ; Sequence 917, Application US/09760469
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PTZ54
 ; CURRENT APPLICATION NUMBER: US/09/760,469
 ; CURRENT FILING DATE: 2001-01-16
 ; PRIOR APPLICATION data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 1983
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 917
 ; LENGTH: 136
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-760-469-917

Query Match 100.0%; Score 675; DB 21; Length 136;
 Best Local Similarity 100.0%; Pred. No. 2.2e-67;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCDAFVGWKLVSSENFDYMKVEGVGFATRKVAGMAKPNMIIISVNGDVTIKSESTFKN 60
 Db 5 MCDAFVGWKLVSSENFDYMKVEGVGFATRKVAGMAKPNMIIISVNGDVTIKSESTFKN 64
 Qy 61 TEISFILGQEFDEVTADRKVKSTITLDGGVLYHVQKWDGKSTTIKRKREDDKLVVECM 120
 Db 65 TEISFILGQEFDEVTADRKVKSTITLDGGVLYHVQKWDGKSTTIKRKREDDKLVVECM 124

Db 65 TEISFILGQEFDEVTADRKVKSTITLDGGVLYHVQKWDGKSTTIKRKREDDKLVVECM 124
 Qy 121 KGVTSTRYERA 132
 Db 125 KGVTSTRYERA 136

RESULT 8
 US-09-760-469-1429
 ; Sequence 1429, Application US/09760469
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PTZ54
 ; CURRENT APPLICATION NUMBER: US/09/760,469
 ; CURRENT FILING DATE: 2001-01-16
 ; PRIOR APPLICATION data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 1983
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 1429
 ; LENGTH: 136
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-760-469-1429

Query Match 100.0%; Score 675; DB 21; Length 136;
 Best Local Similarity 100.0%; Pred. No. 2.2e-67;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCDAFVGWKLVSSENFDYMKVEGVGFATRKVAGMAKPNMIIISVNGDVTIKSESTFKN 60
 Db 5 MCDAFVGWKLVSSENFDYMKVEGVGFATRKVAGMAKPNMIIISVNGDVTIKSESTFKN 64
 Qy 61 TEISFILGQEFDEVTADRKVKSTITLDGGVLYHVQKWDGKSTTIKRKREDDKLVVECM 120
 Db 65 TEISFILGQEFDEVTADRKVKSTITLDGGVLYHVQKWDGKSTTIKRKREDDKLVVECM 124
 Qy 121 KGVTSTRYERA 132
 Db 125 KGVTSTRYERA 136

RESULT 9
 US-09-760-469-1432
 ; Sequence 1432, Application US/09760469
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 ; FILE REFERENCE: PTZ54
 ; CURRENT APPLICATION NUMBER: US/09/760,469
 ; CURRENT FILING DATE: 2001-01-16
 ; PRIOR APPLICATION data removed - consult PALM or file wrapper
 ; NUMBER OF SEQ ID NOS: 1983
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO: 1432
 ; LENGTH: 136
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-760-469-1432

Query Match 100.0%; Score 675; DB 21; Length 136;
 Best Local Similarity 100.0%; Pred. No. 2.2e-67;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCDAFVGWKLVSSENFDYMKVEGVGFATRKVAGMAKPNMIIISVNGDVTIKSESTFKN 60
 Db 5 MCDAFVGWKLVSSENFDYMKVEGVGFATRKVAGMAKPNMIIISVNGDVTIKSESTFKN 64
 Qy 61 TEISFILGQEFDEVTADRKVKSTITLDGGVLYHVQKWDGKSTTIKRKREDDKLVVECM 120
 Db 65 TEISFILGQEFDEVTADRKVKSTITLDGGVLYHVQKWDGKSTTIKRKREDDKLVVECM 124

RESULT 10
 Qy 121 KGVTSTRYERA 132
 |
 | Sequence 1433, Application US/09760469
 | GENERAL INFORMATION:
 | APPLICANT: Rosen et al.
 | TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 | FILE REFERENCE: PTZ54
 | CURRENT APPLICATION NUMBER: US/09/760,469
 | CURRENT FILING DATE: 2001-01-16
 | Prior application data removed - consult PALM or file wrapper
 | NUMBER OF SEQ ID NOS: 1983
 | SOFTWARE: PatentIn Ver. 2.0
 | SEQ ID NO: 1433
 | LENGTH: 136
 | TYPE: PRT
 | ORGANISM: Homo sapiens
 US-09-760-469-1433

Query Match 100.0%; Score 675; DB 21; Length 136;
 Best Local Similarity 100.0%; Pred. No. 2.2e-67;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCDAFVGTVKLVSSENFDYMKVEGYGPATRKVAGMAKPNNMIIISVNGDVITKSESTFKN 60
 Db 5 MCDAFVGTVKLVSSENFDYMKVEGYGPATRKVAGMAKPNNMIIISVNGDVITKSESTFKN 64

Qy 61 TEISFILQEFDETAADDRKVKSITLDDGGVLVHQVKNDGKSTTIKRREDDKLVVECM 120
 Db 65 TEISFILQEFDETAADDRKVKSITLDDGGVLVHQVKNDGKSTTIKRREDDKLVVECM 124

Qy 121 KGVTSTRYERA 132
 Db 125 KGVTSTRYERA 136

RESULT 11
 US-09-760-469-1434
 | Sequence 1434, Application US/09760469
 | GENERAL INFORMATION:
 | APPLICANT: Rosen et al.
 | TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
 | FILE REFERENCE: PTZ54
 | CURRENT APPLICATION NUMBER: US/09/760,469
 | CURRENT FILING DATE: 2001-01-16
 | Prior application data removed - consult PALM or file wrapper
 | NUMBER OF SEQ ID NOS: 1983
 | LENGTH: 136
 | TYPE: PRT
 | ORGANISM: Homo sapiens
 US-09-760-469-1434

Query Match 100.0%; Score 675; DB 21; Length 136;
 Best Local Similarity 100.0%; Pred. No. 2.2e-67;
 Matches 132; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCDAFVGTVKLVSSENFDYMKVEGYGPATRKVAGMAKPNNMIIISVNGDVITKSESTFKN 60
 Db 5 MCDAFVGTVKLVSSENFDYMKVEGYGPATRKVAGMAKPNNMIIISVNGDVITKSESTFKN 64

Qy 61 TEISFILQEFDETAADDRKVKSITLDDGGVLVHQVKNDGKSTTIKRREDDKLVVECM 120
 Db 65 TEISFILQEFDETAADDRKVKSITLDDGGVLVHQVKNDGKSTTIKRREDDKLVVECM 124

RESULT 12
 US-09-834-366-17169
 | Sequence 17169, Application US/09834366
 | GENERAL INFORMATION:
 | APPLICANT: Bejanin, Stephane
 | APPLICANT: Tanaka, Hiroaki
 | APPLICANT: Dumas Milne Edwards, Jean Baptiste
 | APPLICANT: Jober, Sevrin
 | APPLICANT: Giordano, Jean-Yves
 | TITLE OF INVENTION: ESTs and Encoded Human Proteins.
 | FILE REFERENCE: 81.US2.RBG
 | CURRENT APPLICATION NUMBER: US/09/834,366
 | CURRENT FILING DATE: 2001-04-13
 | PRIOR APPLICATION NUMBER: US 60/197,873
 | PRIOR FILING DATE: 2000-04-18
 | NUMBER OF SEQ ID NOS: 52153
 | SOFTWARE: PatentIn.pm
 | SEQ ID NO: 17169
 | LENGTH: 129
 | TYPE: PRT
 | ORGANISM: Homo sapiens
 | FEATURE:
 | NAME/KEY: UNSURE
 | LOCATION: 62
 | OTHER INFORMATION: Xaa = Asp/Glu
 | NAME/KEY: UNSURE
 | LOCATION: 82
 | OTHER INFORMATION: Xaa = Lys/Asn
 US-09-834-366-17169

Query Match 96.1%; Score 649; DB 22; Length 129;
 Best Local Similarity 98.4%; Pred. No. 1.7e-64;
 Matches 127; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MCDAFVGTVKLVSSENFDYMKVEGYGPATRKVAGMAKPNNMIIISVNGDVITKSESTFKN 60
 Db 1 MCDAFVGTVKLVSSENFDYMKVEGYGPATRKVAGMAKPNNMIIISVNGDVITKSESTFKN 60

Qy 61 TEISFILQEFDETAADDRKVKSITLDDGGVLVHQVKNDGKSTTIKRREDDKLVVECM 120
 Db 61 TXSFLQEFDETAADDRKVXSITLDDGGVLVHQVKNDGKSTTIKRREDDKLVVECM 120

Qy 121 KGVTSTRY 129
 Db 121 KGVTSTRY 129

RESULT 13
 US-60-197-873-17169
 | Sequence 17169, Application US/60197873
 | GENERAL INFORMATION:
 | APPLICANT: Bejanin, Stephane
 | APPLICANT: Tanaka, Hiroaki
 | APPLICANT: Dumas Milne Edwards, Jean Baptiste
 | APPLICANT: Jober, Sevrin
 | APPLICANT: Giordano, Jean-Yves
 | TITLE OF INVENTION: ESTs and Encoded Human Proteins.
 | FILE REFERENCE: 81.US1.PRO
 | CURRENT APPLICATION NUMBER: US/60/197,873
 | CURRENT FILING DATE: 2000-04-18
 | NUMBER OF SEQ ID NOS: 52153
 | SOFTWARE: PatentIn.pm
 | SEQ ID NO: 17169
 | LENGTH: 129
 | TYPE: PRT
 | ORGANISM: Homo sapiens
 | FEATURE:

NAME/KEY: UNSURE
 LOCATION: 62
 OTHER INFORMATION: Xaa = Asp, Glu
 NAME/KEY: UNSURE
 LOCATION: 82
 OTHER INFORMATION: Xaa = Lys, Asn
 US-60-197-873-17169

Query Match 96.1%; Score 649; DB 24; Length 129;
 Best Local Similarity 98.4%; Pred. No. 1.7e-64;
 Matches 127; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 SEQ ID NO: 172

QY 1 MCDAFVGTVKLVSSENFDYMKKEYGVGFTRKVAGMAKPNNMISYNGDVITIKSESTFKN 60
 Db 1 MCDAFVGTVKLVSSENFDYMKKEYGVGFTRKVAGMAKPNNMISYNGDVITIKSESTFKN 60

QY 61 TEISPLGQEFDETDADDRKVKSPITLDGGVLVHVQKWDGKSTTIRKRREDDKLVVECYM 120
 Db 61 TXISPLGQEFDETDADDRKVKSPITLDGGVLVHVQKWDGKSTTIRKRREDDKLVVECYM 120

QY 121 KGVTSTRVY 129
 Db 121 KGVTSTRVY 129

RESULT 14
 US-09-503-596-5

Sequence 5, Application US/09503596
 GENERAL INFORMATION:
 APPLICANT: Lee et al.
 TITLE OF INVENTION: Inhibiting formation of Artherosclerotic Lesions
 FILE REFERENCE: 21500-042
 CURRENT APPLICATION NUMBER: US/09/503,596
 CURRENT FILING DATE: 2000-02-11
 PRIOR APPLICATION NUMBER: 60/119,880
 PRIOR FILING DATE: 1999-02-12
 NUMBER OF SEQ ID NOS: 8
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 5
 LENGTH: 132
 TYPE: PRT
 ORGANISM: Mus musculus
 US-09-503-596-5

Query Match 92.6%; Score 625; DB 19; Length 132;
 Best Local Similarity 91.7%; Pred. No. 8.9e-62;
 Matches 121; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 MCDAFVGTVKLVSSENFDYMKKEYGVGFTRKVAGMAKPNNMISYNGDVITIKSESTFKN 60
 Db 1 MCDAFVGTVKLVSSENFDYMKKEYGVGFTRKVAGMAKPNNMISYNGDVITIKSESTFKN 60

QY 61 TEISPLGQEFDETDADDRKVKSPITLDGGVLVHVQKWDGKSTTIRKRREDDKLVVECYM 120
 Db 61 TEISPLGQEFDETDADDRKVKSPITLDGGVLVHVQKWDGKSTTIRKRREDDKLVVECYM 120

QY 121 KGVTSTRVYERA 132
 Db 121 KGVTSTRVYERA 132

RESULT 15
 US-09-699-146-172

Sequence 172, Application US/09699146
 GENERAL INFORMATION:
 APPLICANT: Harukka, Ilkka J
 APPLICANT: Glenn, Matthew
 APPLICANT: Grigor, Murray R.
 APPLICANT: Molenaar, Adrian J.
 TITLE OF INVENTION: Compositions Isolated From Bovine Mammary Gland and Methods For Their Use.

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: January 24, 2002, 09:14:58 ; Search time 11.74 Seconds
(without alignments)
390,957 Million cell updates/sec

Title: US-09-905-235-1

Perfect score: 675 MCDAFYGTWKLYSSENFDYY.....KLVVECYMKGVYSTRYERA 132

Scoring table: BLOSSUM62 Gapop 10.0 , Gapext 0.5

Searched: 160442 seqs, 34711459 residues

Total number of hits satisfying chosen parameters: 160442

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	466	69.0	133	5 US-09-901-436-7	Sequence 7, Appl
2	463	68.6	132	5 US-09-901-436-11	Sequence 11, Appl
3	449	66.5	133	5 US-09-901-436-10	Sequence 10, Appl
4	445	65.9	132	5 US-09-986-240-2	Sequence 2, Appl
5	399	59.1	132	5 US-09-971-187-2	Sequence 2, Appl
6	225	33.3	134	5 US-09-901-436-9	Sequence 9, Appl
7	212	31.4	135	5 US-09-901-436-8	Sequence 8, Appl
8	201.5	29.9	138	6 US-10-017-754-328	Sequence 328, Appl
9	122	18.1	107	5 US-09-901-436-2	Sequence 2, Appl
10	86	12.7	127	5 US-09-981-353-1	Sequence 21, Appl
11	74.5	11.0	304	5 US-09-620-394B-4280	Sequence 4280, Ap
12	74.5	11.0	547	5 US-09-708-427-20771	Sequence 20771, A
13	74.5	11.0	559	5 US-09-708-427-20770	Sequence 20770, A
14	74.5	11.0	610	5 US-09-815-242-13176	Sequence 13176, A
15	74.5	11.0	662	5 US-09-708-427-20769	Sequence 20769, A
16	69.5	10.3	380	5 US-09-708-427-21665	Sequence 21665, A
17	69.5	10.3	446	5 US-09-708-427-21665	Sequence 21665, A
18	69.5	10.3	510	5 US-09-708-427-21664	Sequence 21664, A
19	69	10.2	380	5 US-09-708-427-35496	Sequence 35496, A
20	69	10.2	446	5 US-09-708-427-35495	Sequence 35495, A
21	69	10.2	510	5 US-09-971-776-2	Sequence 2, Appl
22	69	10.2	511	5 US-09-708-427-35494	Sequence 35494, A
23	68	10.1	247	7 US-09-331-358-579	Sequence 579, Ap
24	67.5	10.0	240	5 US-09-815-242-13453	Sequence 13453, A
25	67.5	10.0	241	5 US-09-815-242-13609	Sequence 13609, A
26	67.5	10.0	361	5 US-09-708-427-58892	Sequence 58892, A

RESULT 1
US-09-901-436-7

Sequence 7, Application US/09901436

GENERAL INFORMATION:

APPLICANT: Ni, Jian Gentz, Reiner Yu, Guo-Liang Rosen, Craig A

TITLE OF INVENTION: Cytostatin I

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: HUNAN GENOME SCIENCES, INC.

STREET: 9410 KEY WEST AVENUE

CITY: ROCKVILLE

STATE: MARYLAND

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/901,436

FILING DATE: 10-Jul-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/361,737

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Wales, Michele M.

REGISTRATION NUMBER: P-43,975

REFERENCE/DOCKET NUMBER: PF175D2

TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-610-5772

TELEFAX: 301-309-8439

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 133 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-09-901-436-7

Matches 89; Conservative 15; Mismatches 27; Indels 0; Gaps 0; QY 1 MCDAFGTWKLVSSENEDDMKEYGVGATRKVAGMAKPNMISVNGDVITIKSESTFKN 60
Db 1 MADAFVGTVWKLVDSDKNFDDMKSIGVGFATRVOASMTKPTTLEKNGDTITKQSTFKN 60

RESULT 3
US-09-901-436-10 ; Sequence 10, Application US/09901436
GENERAL INFORMATION:
APPLICANT: Ni, Jian
Gentz, Reiner
Yu, Guo-Liang
Rosen, Craig A

TITLE OF INVENTION: Cystostatin I
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MARYLAND
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/901,436
FILING DATE: 10-JUL-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/361,737
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Wales, Michele M.

TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5772
TELEFAX: 301-309-8439

INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-901-436-10

Query Match 66.5%; Score 449; DB 5;
Best Local Similarity 64.9%; Pred. No. 1.2e-36;
Matches 85; Conservative 16; Mismatches 30; Indels 0; Gaps 0;

QY 1 MCDAFGTVWKLVDSDKNFDDMKSIGVGFATRVOASMTKPTTLEKNGDTITKQSTFKN 60
Db 1 MADAFVGTVWKLVDSDKNFDDMKSIGVGFATRVOASMTKPTTLEKNGDTITKQSTFKN 60

RESULT 4
US-09-986-240-2 ; Sequence 2, Application US/09986240
GENERAL INFORMATION:
APPLICANT: Ni, Jian
Gentz, Reiner
Yu, Guo-Liang
Rosen, Craig A

TITLE OF INVENTION: Cystostatin I
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MARYLAND
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/901,436
FILING DATE: 10-JUL-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/361,737
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Wales, Michele M.
REGISTRATION NUMBER: P-43,975
REFERENCE/DOCKET NUMBER: PF115D2

TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5772
TELEFAX: 301-309-8439

INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 11:
US-09-901-436-11

Query Match 68.6%; Score 463; DB 5;
Best Local Similarity 67.2%; Pred. No. 5e-38;
Matches 88; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

QY 1 MCDAFGTVWKLVDSDKNFDDMKSIGVGFATRVOASMTKPTTLEKNGDTITKQSTFKN 60
Db 1 MADAFVGTVWKLVDSDKNFDDMKSIGVGFATRVOASMTKPTTLEKNGDTITKQSTFKN 60

RESULT 5
US-09-986-240-3 ; Sequence 3, Application US/09986240
GENERAL INFORMATION:
APPLICANT: Ni, Jian
Gentz, Reiner
Yu, Guo-Liang
Rosen, Craig A

TITLE OF INVENTION: Cystostatin I
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MARYLAND
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/901,436
FILING DATE: 10-JUL-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/361,737
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Wales, Michele M.
REGISTRATION NUMBER: P-43,975
REFERENCE/DOCKET NUMBER: PF115D2

TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5772
TELEFAX: 301-309-8439

INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-09-901-436-12

Query Match 66.5%; Score 449; DB 5;
Best Local Similarity 64.9%; Pred. No. 1.2e-36;
Matches 85; Conservative 16; Mismatches 30; Indels 0; Gaps 0;

QY 1 MCDAFGTVWKLVDSDKNFDDMKSIGVGFATRVOASMTKPTTLEKNGDTITKQSTFKN 60
Db 1 MADAFVGTVWKLVDSDKNFDDMKSIGVGFATRVOASMTKPTTLEKNGDTITKQSTFKN 60

RESULT 6
US-09-986-240-4 ; Sequence 4, Application US/09986240
GENERAL INFORMATION:
APPLICANT: Ni, Jian
Gentz, Reiner
Yu, Guo-Liang
Rosen, Craig A

TITLE OF INVENTION: Cystostatin I
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MARYLAND
COUNTRY: USA
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/901,436
FILING DATE: 10-JUL-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/361,737
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Wales, Michele M.
REGISTRATION NUMBER: P-43,975
REFERENCE/DOCKET NUMBER: PF115D2

TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-610-5772
TELEFAX: 301-309-8439

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-09-901-436-13

Query Match 66.5%; Score 449; DB 5;
Best Local Similarity 64.9%; Pred. No. 1.2e-36;
Matches 85; Conservative 16; Mismatches 30; Indels 0; Gaps 0;

QY 1 MCDAFGTVWKLVDSDKNFDDMKSIGVGFATRVOASMTKPTTLEKNGDTITKQSTFKN 60
Db 1 MADAFVGTVWKLVDSDKNFDDMKSIGVGFATRVOASMTKPTTLEKNGDTITKQSTFKN 60

GENERAL INFORMATION:
; APPLICANT: Weigelt, Johan
; TITLE OF INVENTION: NEW NUCLEAR MAGNETIC RESONANCE SCREENING
; TITLE OF INVENTION: METHOD
; FILE REFERENCE: 13425-047001
; CURRENT APPLICATION NUMBER: US/09/986, 240
; CURRENT FILING DATE: 2001-10-19
; PRIOR APPLICATION NUMBER: 60/243, 626
; PRIOR FILING DATE: 2000-10-26
; PRIOR APPLICATION NUMBER: SE 0003811-7
; PRIOR FILING DATE: 2000-10-20
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-986-240-2

Query Match 65.9%; Score 445; DB 5; Length 132;
Best Local Similarity 65.1%; Pred. No. 2.8e-36;
Matches 80; Conservative 16; Mismatches 29; Indels 0; Gaps 0;
Qy 3 DAFVGTWKLYSENFDYMKVEGVGFATRKVAGMAKPNMTISNGDVTIKSESTFEKNT 62
Db 2 DAFUGTWKLYSDKNFDDTMKSLGVGFATRQASMTKPTIIEKGDLTLKHSTFEKNT 61
Qy 63 ISFLGQEFDEVADDRKVKSITLDGGYLHVQKWDGKSTTKRKREDDKLIVVECVMKG 122
Db 62 ISFLKLGVFEDDEVADDRKVKSITLDGSKLHVQKWDQETVLRELIDGKLILTLHGT 121
Qy 123 VSTRYER 131
Db 122 AVCTRTRYEK 130

RESULT 5
US-09-971-187-2
; Sequence 2, Application US/09971187
; GENERAL INFORMATION:
; APPLICANT: Jian Ni et al.
; TITLE OF INVENTION: Cytostatin II
; FILE REFERENCE: PE221D1
; CURRENT APPLICATION NUMBER: US/09/971, 187
; CURRENT FILING DATE: 2001-10-05
; PRIOR APPLICATION NUMBER: 09/043, 646
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: PCT/US95/12540
; PRIOR FILING DATE: 1995-09-25
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 2
; LENGTH: 132
; TYPE: PRT
; ORGANISM: human
US-09-971-187-2

Query Match 59.1%; Score 399; DB 5; Length 132;
Best Local Similarity 56.8%; Pred. No. 8.1e-32;
Matches 75; Conservative 21; Mismatches 36; Indels 0; Gaps 0;
Qy 1 MCDAFGTWKLYSENFDYMKVEGVGFATRKVAGMAKPNMTISNGDVTIKSESTFEK 60
Db 1 MYEARCATWKLNQNDEYMAKLGVEFATRQGNTVKPTVLSQEGDKVWVRLTEFKN 60

Query Match 59.1%; Score 399; DB 5; Length 132;
Best Local Similarity 56.8%; Pred. No. 8.1e-32;
Matches 75; Conservative 21; Mismatches 36; Indels 0; Gaps 0;
Qy 61 TETSFILGQEFDEVADDRKVKSITLDGGYLHVQKWDGKSTTKRKREDDKLIVVECVM 120
Db 61 TEISFQLGEEFDETTADRNCSVSVSLDGDKLVHIOQWDGKLTNFREIKOGMMWMLTF 120
Qy 121 KGYTSTRYER 132

Db 121 GDVVAVRHEKA 132
RESULT 6
US-09-901-436-9
; Sequence 9, Application US/09901436
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; Gentz, Peiner
; Yu, Guo-Liang
; Rosen, Craig A
; TITLE OF INVENTION: Cytostatin I
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/901,436
; FILING DATE: 10-Jul-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/361,737
; REFERENCE/DOCKET NUMBER: PF175D2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 301-610-5772
; TELEFAX: 301-309-8439
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 134 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-901-436-9

Query Match 33.3%; Score 225; DB 5; Length 134;
Best Local Similarity 38.6%; Pred. No. 6.3e-15;
Matches 49; Conservative 27; Mismatches 49; Indels 2; Gaps 1;
Qy 7 GTWKLYSENFDYMKVEGVGFATRKVAGMAKPNMTISNGDVTIKSESTFEKNT 66
Db 7 GTWMESENFDYMKVEGVGFATRKVAGMAKPNMTISNGDVTIKSESTFEKNT 66
Qy 67 LGQEFDEVV-ADDRKVKSITLDGGYLHVQKWDGKSTTKRKREDDKLIVVECVMKG 124
Db 67 GTWMESENFDYMKVEGVGFATRKVAGMAKPNMTISNGDVTIKSESTFEKNT 66
Qy 125 STRYER 131
Db 127 CRQVFKK 133
RESULT 7
US-09-901-436-8
; Sequence 8, Application US/09901436
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian

Gentz, Reiner
 Yu, Guo-Liang
 Rosen, Craig A.

TITLE OF INVENTION: Cytostatin I

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: HUMAN GENOME SCIENCES, INC.

CITY: ROCKVILLE

STATE: MARYLAND

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30

APPLICATION NUMBER: US/09/901,436

FILING DATE: 10-JUL-2001

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/361,737

FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Wales, Michelle M.

REGISTRATION NUMBER: P-43,975

REFERENCE/DOCKET NUMBER: PFI175D2

TELEPHONE: 301-610-5772

TELEFAX: 301-309-8439

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 135 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: Linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 8:
 US-09-901-436-8

Query Match 31.4%; Score 212; DB 5; Length 135;
 Best Local Similarity 35.7%; Pred. No. 1.2e-13;
 Matches 46; Conservative 34; Mismatches 47; Indels 2; Gaps 1;

QY 5 FVGTWKLYSSENNDDYMEKVGFAFRK--VAGMAKMINIISVNGDYTIKSESTFKNTI 62
 DB 5 FGTYWKLYSSENNDDYMEKVGFAFRK--VAGMAKMINIISVNGDYTIKSESTFKNTI 62

QY 63 ISPLGQEFDEVTADDRKVKSITLDGVLYHIVQKWDG-----KSTIK 106
 DB 64 INFKVGEFFEEQFDGRCKSLV-----KWESENKAQEQLKLKGEGPKTSWTR 112

RESULT 9
 US-09-901-436-2

Sequence 2, Application US/09/901,436

GENERAL INFORMATION:

APPLICANT: Ni, Jian
 Gentz, Reiner
 Yu, Guo-Liang
 Rosen, Craig A.

TITLE OF INVENTION: Cytostatin I

NUMBER OF SEQUENCE: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: HUMAN GENOME SCIENCES, INC.

STREET: 9410 KEY WEST AVENUE
 CITY: ROCKVILLE
 STATE: MARYLAND
 COUNTRY: USA
 ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DO/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/901,436
 FILING DATE: 10-JUL-2001
 CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/361,737

ATTORNEY/AGENT INFORMATION:

NAME: Wales, Michele M.
 REGISTRATION NUMBER: P-43,975
 REFERENCE/DOCKET NUMBER: PFI175D2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 301-610-5772
 TELEX: 301-309-8439

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 107 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 2:
 US-09-901-436-2

Query Match 18.1%; Score 122; DB 5; Length 107;
 Best Local Similarity 33.8%; Pred. No. 4.7e-05;
 Matches 23; Conservative 20; Mismatches 25; Indels 0; Gaps 0;

QY 7 GTWKLYSSENFFDDYMKEVGVFATRKVAGMAKPNMIIISYNGDVITIKSESTFKTEISFI 66
 Db 7 GYRVEVSQKMDYLQALNISLAVRKIALLKPDKEIEHOGNNHTVRTLSFRNTLQED 66
 QY 67 LGQEFDEV 74
 Db 67 VGVGEV 74

RESULT 10
 US-09-981-353-21
 Sequence 21. Application US/09981353
 GENERAL INFORMATION:
 APPLICANT: Lasek, Amy W.
 TITLE OF INVENTION: GENES EXPRESSED IN COLON CANCER
 CURRENT APPLICATION NUMBER: US/09/981,353
 CURRENT FILING DATE: 2001-10-11
 NUMBER OF SEQ ID NOS: 194
 SOFTWARE: PERL Program
 SEQ ID NO 21
 LENGTH: 127
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 NAME/KEY: misc_feature
 OTHER INFORMATION: Incyte ID No: 1282225CD1
 US-09-981-353-21

Query Match 12.7%; Score 86; DB 5; Length 127;
 Best Local Similarity 26.0%; Pred. No. 0.18;
 Matches 26; Conservative 17; Mismatches 29; Indels 28; Gaps 3;

QY 4 AFVGTVKLYSSENFFDDYMKEVGVFATRKVAGMAKPNMIIISYNGDV----- 49
 Db 2 SFGKYQLQSQNEFAFMKAIG-----PEELIQGKDTRKGVSEIYQNGKHEK 49
 QY 50 ITKSESTFKTEISFLQEFDEVADRKVYSTITLDG 89
 Db 50 FTTAGS-KVYONEEYVGECELEMTGKVTVNQLEG 87

RESULT 11
 US-09-620-394B-4280
 Sequence 4280, Application US/09620394B
 GENERAL INFORMATION:
 APPLICANT: ALEXANDROV, Nickolai
 APPLICANT: BROVER, Vyacheslav
 TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 TITLE OF INVENTION: Thereby
 FILE REFERENCE: 2750-1057P
 CURRENT APPLICATION NUMBER: US/09/620,394B
 CURRENT FILING DATE: 2000-07-21
 NUMBER OF SEQ ID NOS: 9131
 SEQ ID NO 4280
 LENGTH: 304
 TYPE: PRT
 ORGANISM: Arabidopsis thaliana
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1..304
 OTHER INFORMATION: Xaa is any amino acid

NAME/KEY: misc_feature
 LOCATION: 1..304
 OTHER INFORMATION: Ceres Seq. ID 1388881
 OTHER INFORMATION: US-09-620-394B-4280

Query Match 11.0%; Score 74.5; DB 5; Length 304;
 Best Local Similarity 25.0%; Pred. No. 7.3;
 Matches 36; Conservative 19; Mismatches 54; Indels 35; Gaps 6;

QY 3 DAFVGTVKLYSSENFFDDYMKEVGVFATRKVAGMAKPNMIIISYNGDVITIKS----- 54
 Db 152 EAFTSGCTTIVSKYVNLSEATTD-ELKTTFQCGYGSQRYGTFQDFTKDSAK-NAIEKLNGKVNDKQ1FVGDFL 210
 QY 55 -----ESTFKTEISFLQEFDEVADRKVYSTITLDGKV-LVHVKWGDKS----- 102
 Db 211 RKEERESAADMKEFVNYYVKNLSEATTD-ELKTTFQCGYGSQSSAVMRDGDKSRCSRCGF 269
 QY 103 -----TTIKRKREDDK 113
 Db 270 VNENPENPDAARAVEALNKKFDDK 293

RESULT 12
 US-09-708-427-20771
 Sequence 20771, Application US/09708427
 GENERAL INFORMATION:
 APPLICANT: N ALEXANDROV et al.
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDE
 FILE OF INVENTION: THEREBY
 FILE REFERENCE: 2750-1243P
 CURRENT APPLICATION NUMBER: US/09/708,427
 CURRENT FILING DATE: 2000-11-09
 NUMBER OF SEQ ID NOS: 85364
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 20771
 LENGTH: 547
 TYPE: PRT
 ORGANISM: Arabidopsis thaliana
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1..547
 OTHER INFORMATION: Xaa is any amino acid
 NAME/KEY: misc_feature
 LOCATION: 1..547
 OTHER INFORMATION: Ceres Seq. ID 1838598
 US-09-708-427-20771

Query Match 11.0%; Score 74.5; DB 5; Length 547;
 Best Local Similarity 25.0%; Pred. No. 16;
 Matches 36; Conservative 19; Mismatches 54; Indels 35; Gaps 6;

QY 3 DAFVGTVKLYSSENFFDDYMKEVGVFATRKVAGMAKPNMIIISYNGDVITIKS----- 54
 Db 37 EAFTSGCTTIVSKYVNLSEATTD-ELKTTFQCGYGSQRYGTFQDFTKDSAK-NAIEKLNGKVNDKQ1FVGFL 95
 QY 55 -----ESTFKTEISFLQEFDEVADRKVYSTITLDGKV-LVHVKWGDKS----- 102
 Db 96 RKEERESAADMKEFVNYYVKNLSEATTD-ELKTTFQCGYGSQSSAVMRDGDKSRCSRCGF 154
 QY 103 -----TTIKRKREDDK 113
 Db 155 VNENPENPDAARAVEALNKKFDDK 178

RESULT 13
 US-09-708-427-20770
 Sequence 20770, Application US/09708427
 GENERAL INFORMATION:
 APPLICANT: N ALEXANDROV et al.
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDE
 FILE OF INVENTION: THEREBY

FILE REFERENCE: 2750-1243P
 CURRENT APPLICATION NUMBER: US/09/708,427
 CURRENT FILING DATE: 2000-11-09
 NUMBER OF SEQ ID NOS: 85364
 SOFTWARE: Patentin version 3.1
 SEQ ID NO: 20770
 LENGTH: 539
 TYPE: PRT
 ORGANISM: Arabidopsis thaliana
 FEATURE: misc_feature
 NAME/KEY: misc_feature
 LOCATION: 1..559
 OTHER INFORMATION: Xaa is any amino acid
 NAME/KEY: misc_feature
 LOCATION: 1..559
 OTHER INFORMATION: Ceres Seq. ID 1838597
 US-09-708-427-20770

RESULT 14
 Query Match 11.0%; Score 74.5; DB 5; Length 559;
 Best Local Similarity 25.0%; Pred. No. 16; Mismatches 54; Indels 35; Gaps 6;
 Matches 36; Conservative 19; Mismatches 54; Indels 35; Gaps 6;
 QY 3 DAFYGTWKLVSSENFDYDM-KEYVGFATRKVAGMAKPKNMISVNGDVTIKS-----
 Db 49 EAFSGCGTIVSKCKVATDHMQSRSQGYFQDTESAK-NAIEKINGKVINDKQIFVGPFEL 107
 QY 55 -----ESTKNTESFLIGQEFDEVTDARKVSTITLDGGV-LVHYQKDGS----- 102
 Db- 108 RKEERESAADKMKTINVYVKNLSEATTDD-ELKTFEGQYGSISSAVMRDGDKSRCFG 166
 QY 103 -----TTIKRREDDK 113
 Db 167 VNFENPEDARAAVEALNGKKFDDK 190

GENERAL INFORMATION:
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohisen, Kari L.
 APPLICANT: Zyskind, Judith W.
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John D.
 APPLICANT: Carr, Grant J.
 APPLICANT: Yamamoto, Robert T.
 APPLICANT: Xu, H. Howard
 TITLE OF INVENTION: Identification of Essential Genes in
 TITLE OF INVENTION: Prokaryotes
 FILE REFERENCE: ELITRA.011A
 CURRENT APPLICATION NUMBER: US/09/815,242
 CURRENT FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-16
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 NUMBER OF SEQ ID NOS: 14110
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 13176
 LENGTH: 610
 TYPE: PRT
 ORGANISM: Streptococcus pneumoniae

US-09-815-242-13176
 Query Match 11.0%; Score 74.5; DB 5; Length 610;
 Best Local Similarity 30.3%; Pred. No. 18;
 Matches 27; Conservative 15; Mismatches 40; Indels 7; Gaps 3;
 Qy 21 MKEVGVPATRKVAGMAKPKNMISVNGDVTIKS-----
 Db 447 MQKVHAGLAVD-TGVEDNIFMSNGDLAFTADSARIAGHENAQDIYVDGNRIGEGA 504
 QY 77 DDRKVKSITLDDGVLVHVQKDGSKSTI 105
 Db 505 AVLKDRLDSEGVLA-VATVDFKSQMI 532

RESULT 15
 US-09-708-427-20769
 Sequence 20769, Application US/09708427
 GENERAL INFORMATION:
 APPLICANT: N ALEXANDROV et al
 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
 FILE REFERENCE: THE REB
 CURRENT APPLICATION NUMBER: US/09/708,427
 CURRENT FILING DATE: 2000-11-09
 NUMBER OF SEQ ID NOS: 85364
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 20769
 LENGTH: 662
 TYPE: PRT
 ORGANISM: Arabidopsis thaliana
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: 1..662
 OTHER INFORMATION: Xaa is any amino acid
 NAME/KEY: misc_feature
 LOCATION: 1..662
 OTHER INFORMATION: Ceres Seq. ID 1838596
 US-09-708-427-20769

Query Match 11.0%; Score 74.5; DB 5; Length 662;
 Best Local Similarity 25.0%; Pred. No. 20; Mismatches 19; Indels 35; Gaps 6;
 Matches 36; Conservative 19; Mismatches 54; Indels 35; Gaps 6;
 Qy 3 DAFVGTVKLVSSENFDVM-KEVGVGFTRKVAGMAKPKNMISVNGDVTIKS-----
 Db 152 EAFFGGCTIVSKCKVATDHMQSRSQGYFQDTESAK-NAIEKINGKVINDKQIFVGPFEL 210
 Qy 55 -----ESTKNTESFLIGQEFDEVTDARKVSTITLDGGV-LVHYQKDGS----- 102
 Db 211 RKEERESAADKMKTINVYVKNLSEATTDD-ELKTFEGQYGSISSAVMRDGDKSRCFG 269
 Qy 103 -----TTIKRREDDK 113
 Db 270 VNFENPEDARAAVEALNGKKFDDK 293

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scoring table:	BLOSUM62								
Gapop:	10.0 , Gapext 0.5								
searched:	219241 seqs, 76174552 residues								
total number of hits satisfying chosen parameters:	219241								
minimum DB seq length:	0								
maximum DB seq length:	2000000000								
Post-processing: Minimum Match 08 Maximum Match 100% Listing first 45 summaries									
database :	PIR_68;*								
	1: pir1:*								
	2: pir2:*								
	3: pir3:*								
	4: pir4:*								
• Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.									
SUMMARIES									
result No.	Score	Match Length	DB	ID	Description				
1	675	100.0	132	1 FZHFU	fatty acid-binding				
2	623	92.3	132	2 B25552	myelin P2 protein				
3	578	85.6	132	2 S57744	adipocyte-type fat				
4	486	72.0	132	1 MPRB2	myelin P2 protein				
5	477	70.7	133	2 A27452	fatty acid-binding				
6	466	69.0	133	2 PC4011	myelin P2 protein				
7	463	68.6	132	1 MPHU2	fatty acid-binding				
8	450	66.7	132	2 JH0407	myelin P2 protein				
9	450	66.5	133	2 FZHDU	fatty acid-binding				
10	448	66.4	131	1 MPBD2	myelin P2 protein				
11	446	66.1	133	2 A34676	fatty acid-binding				
12	425	63.0	131	2 S06179	fatty acid-binding				
13	392	58.1	132	2 A49184	fatty acid-binding				
14	390	57.8	132	2 I52324	testis lipid bindi				
15	381	57.0	132	2 I56510	fatty acid binding				
16	381	56.4	132	2 I58161	lipid-binding prot				
17	381	56.4	132	2 I4823	hypothetical prote				
18	378	56.0	132	2 S20397	hypothetical prote				
19	366	54.2	135	2 I50326	fatty acid binding				
20	362	53.6	135	2 A41497	fatty acid binding				
21	361	53.5	135	2 JC2201	lipid-binding prot				
22	307	45.6	135	2 T15205	fatty acid-binding				
23	300.5	44.5	136	2 T15207	hypothetical prote				
24	265.5	38.0	137	2 T25123	hypothetical prote				
25	242.5	35.9	133	2 A48578	fatty acid-binding				
26	241.5	34.3	134	2 S29600	fatty acid-binding				
27	239.5	34.0	133	2 A39818	4K fatty acid-bin				
28	227	33.6	133	2 A49870	retinol-binding pr				
29	227	33.6	134	2 S3417	fatty acid-binding				

J. Biol. Chem.	261, 10821-10827, 1986	QY 61 TEISFLGQEFDEVTDKVKSTTILDGGLVQKWDGKSTTIIKKREDDKLVVECM 120
A; Title:	the nucleotide sequence of three genes participating in the adipose differentiation	Db 61 TEISFLGQEFDEVTDKVKSTTILDGGLVQKWDGKSTTIIKKREDDKLVVECM 120
A; Reference number:	A92553;	
A; Accession:	B25952	
A; Molecule type: DNA		
A; Residues: 1-132 <P2>		
A; Cross-references: GB:MI3385; NID:9198718; PIDN:AAA39416.1; PID:9387401		
A; Note: the authors translated the codon GTG for residue 111 as Gly		
R; Bansal, M.P.; Medina, D.		
Biochem. Biophys. Res. Commun.	191, 61-69, 1983	
A; Expression of fatty acid-binding proteins in the developing mouse mammary gland		
A; Reference number: PC1249		
A; Molecule type: protein		
A; Residues: 25-35;37-51;59-88 <BAN>		
A; Experimental source: mammary gland		
R; Hunt, C.R.; Ro, J.H.S.; Dobson, D.E.; Min, H.Y.; Spiegelman, B.M.		
Proc. Natl. Acad. Sci. U.S.A.	83, 3786-3790, 1986	
A; Title: Adipocyte P2 gene: Developmental expression and homology of 5'-flanking sequence		
A; Reference number: A24884;		
A; Accession: A24884		
A; Molecule type: DNA		
A; Residues: 1-39, 'T, '41-110, 'G, '112-132 <HUN>		
A; Cross-references: GB:MI1264; NID:200113; PIDN:AAA39870.1; PID:9387504		
A; Note: the authors translated the codon ACC for residue 40 as Ser		
R; Bernlohr, D.A.; Angus, C.W.; Lane, M.D.; Bolanowski, M.A.; Kelly Jr., T.J.		
Proc. Natl. Acad. Sci. U.S.A.	81, 5468-5472, 1984	
A; Title: Expression of specific mRNAs during adipose differentiation: identification of		
A; Reference number: A05089; MUID:84298159		
A; Accession: A05089		
A; Molecule type: mRNA		
A; Residues: 1-110, 'G, '112-132 <BBR>		
A; Cross-references: GB:K02109; NID:9198716; PIDN:AAA39416.1; PID:9293695		
R; Matarese, V.; Bernlohr, D.A.		
J. Biol. Chem.	263, 14544-14551, 1988	
A; Title: Purification of murine adipocyte lipid-binding Protein. Characterization as a		
A; Reference number: A30810; MUID:89008309		
A; Accession: A30810		
A; Molecule type: protein		
A; Residues: 2-110, 'G, '112-132 <MAT>		
R; Cook, K.; Hunt, C.R.; Spiegelman, B.M.		
J. Cell. Biol.	100, 514-520, 1985	
A; Title: Developmentally regulated mRNAs in 3T3-adipocytes: Analysis of transcriptional		
A; Reference number: I49440; MUID:85105214		
A; Accession: I49440		
A; Status: translated from GB/EMBL/DBJ		
A; Molecule type: mRNA		
A; Residues: 11-110, 'G, '112-132 <RES>		
A; Cross-references: GB:MI28726; NID:9191492; PIDN:AAA37112.1; PID:9191493		
R; Cook, J.S.; Lucas, J.J.; Sibley, E.; Bolanowski, M.A.; Christy, R.J.; Kelly, T.J.; Larson, S.		
Proc. Natl. Acad. Sci. U.S.A.	85, 2949-2953, 1988	
A; Title: Expression of the differentiation-induced gene for fatty acid-binding protein 1		
A; Reference number: I49467; MUID:88203618		
A; Accession: I49467		
A; Status: translated from GB/EMBL/DBJ		
A; Molecule type: DNA		
A; Residues: 1-11 <RE2>		
A; Cross-references: GB:MI20497; NID:9191743; PIDN:AAA37188.1; PID:9191744		
A; Experimental source: 3T3-L1 cells		
A; Introns: 25/1; 82/3; 116/3		
C; Superfamily: myelin P2 protein		
C; Keywords: lipid binding; phosphoprotein		
Query Match 92.3%; Score 623; DB 2; Length 132;		
Best Local Similarity 91.7%; Pred. No. 8.6e-50;		
Matches 121; Conservative 5; Mismatches 6; Indels 0; Gaps 0;		
Db 1 MCDAFVGTVKLVSSENFDYMEKVGVGFATRKVAGMAKPNMITSNGDVITIKSESTFKN 60		
Db 1 MCDAFVGTVKLVSSENFDYMEKVGVGFATRKVAGMAKPNMITSNGDVITIKSESTFKN 60		
QY 1 MCDAFVGTVKLVSSENFDYMEKVGVGFATRKVAGMAKPNMITSNGDVITIKSESTFKN 60		
Db 1 MCDAFVGTVKLVSSENFDYMEKVGVGFATRKVAGMAKPTLTSNLNGVYTSESTFKN 60		
QY 61 TEISFLGQEFDEVTDKVKSTTILDGGLVQKWDGKSTTIIKKREDDKLVVECM 120		
Db 61 TEISFLGQEFDEVTDKVKSTTILDGGLVQKWDGKSTTIIKKREDDKLVVECM 120		
RESULT 3		
C; Species: Bos primigenius taurus (cattle)		
C; Date: 19-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 13-Aug-1999		
C; Accession: S57744		
R; Specht, B.; Bartetzko, N.; Kuhl, H.; Franke, R.; Boerchers, T.; Spener, F.		
submitted to the EMBL Data Library, June 1995		
A; Description: Mammary derived growth inhibitor - not a distinct protein but a mix of		
A; Reference number: S57744		
A; Status: preliminary		
A; Molecule type: mRNA		
A; Residues: 1-132 <SPE>		
A; Cross-references: EMBL:X89244; NID:9895753; PIDN:CAA61532.1; PID:9895754		
C; Superfamily: myelin P2 protein		
Query Match 85.6%; Score 578; DB 2; Length 132;		
Best Local Similarity 84.1%; Pred. No. 1.1e-45;		
Matches 111; Conservative 8; Mismatches 13; Indels 0; Gaps 0;		
QY 1 MCDAFVGTVKLVSSENFDYMEKVGVGFATRKVAGMAKPNMITSNGDVITIKSESTFKN 60		
Db 1 MCDAFVGTVKLVSSENFDYMEKVGVGFATRKVAGMAKPTLTSNLNGVYTSESTFKN 60		
QY 61 TEISFLGQEFDEVTDKVKSTTILDGGLVQKWDGKSTTIIKKREDDKLVVECM 120		
Db 61 TEISFLGQEFDEVTDKVKSTTILDGGLVQKWDGKSTTIIKKREDDKLVVECM 120		
RESULT 4		
MPPB2		
myelin P2 protein - rabbit		
C; Species: Oryctolagus cuniculus (domestic rabbit)		
C; Date: 30-Jun-1990 #sequence_revision 10-May-1996 #text_change 22-Jun-1999		
C; Accession: A28081; AA266; A92372; A03145		
R; Narayanan, V.; Barbosa, E.; Reed, R.; Tennekoos, G.		
J. Biol. Chem.	263, 8332-8337, 1988	
A; Title: Characterization of a cloned cDNA encoding rabbit myelin P-2 protein.		
A; Reference number: A28081; MUID:88228063		
A; Accession: A28081		
A; Molecule type: mRNA		
A; Residues: 1-132 <NAR>		
A; Cross-references: GB:J03744; NID:9165657; PIDN:AAA31451.1; PID:9165658		
A; Note: translation of initiator Met is not shown		
R; Ishaque, A.; Hofmann, T.; Rhee, S.; Eylar, E.H.		
J. Biol. Chem.	255, 1058-1063, 1980	
A; Title: The NH-2-terminal region of the P2 protein from rabbit sciatic nerve myelin.		
A; Reference number: A92372; MUID:8094496		
A; Accession: A92266		
A; Molecule type: protein		
A; Residues: 2-56 <IS1>		
R; Ishaque, A.; Hofmann, T.; Eylar, E.H.		
J. Biol. Chem.	257, 592-595, 1982	
A; Title: The complete amino acid sequence of the P2 protein		
A; Reference number: A92372; MUID:8098098		
A; Accession: A92266		
A; Molecule type: protein		
A; Residues: 56-722 <IS2>		
Db 1 MCDAFVGTVKLVSSENFDYMEKVGVGFATRKVAGMAKPNMITSNGDVITIKSESTFKN 60		
Db 1 MCDAFVGTVKLVSSENFDYMEKVGVGFATRKVAGMAKPNMITSNGDVITIKSESTFKN 60		
QY 1 MCDAFVGTVKLVSSENFDYMEKVGVGFATRKVAGMAKPNMITSNGDVITIKSESTFKN 60		
Db 1 MCDAFVGTVKLVSSENFDYMEKVGVGFATRKVAGMAKPNMITSNGDVITIKSESTFKN 60		

C;Comment: P2 protein and myelin basic protein together constitute a major fraction of p
 C;Superfamily: myelin P2 protein
 C;Keywords: acetylated amino end; myelin; phosphoprotein
 F;2/Nmodified site: acetylated amino end (Ser) (in mature form) #status experimental
 F;2/Binding site: phosphate (Tyr) (covalent) #status predicted
 F;118-125/Disulfide bonds: #status predicted

R;Kanda, T.; Iseki, S.; Hitomi, M.; Kimura, H.; Odani, S.; Kondo, H.; Matsubara, Y.;
 Eur. J. Biochem. 185, 27-33, 1989
 A;Title: Purification and characterization of a fatty-acid-binding protein from the g
 A;Reference number: S06478; MUID:90032682
 A;Accession: S06478
 A;Molecule type: protein
 A;Residues: 1-133 <KAN>
 A;Experimental source: stomach
 R;Jones, P.D.; Carne, A.; Bass, N.M.; Grigor, M.R.
 Biochem. J. 251, 919-925, 1988
 A;Title: Isolation and characterization of fatty acid binding proteins from mammary t
 A;Reference number: S02471; MUID:8832235
 A;Accession: S02471
 A;Molecule type: protein
 A;Residues: 16-22-32-45; 54-59, 'XX', 62-63, 'X', 65-70; 83-93; 97-107; 117-127 <JON>
 A;Experimental source: strain Wistar; mammary
 C;Superfamily: myelin P2 protein
 C;Keywords: acetylated amino end; cardiac muscle; heart; lipid binding; phosphoprotein
 F;1-133;Product: fatty c1d-binding protein #status experimental <MT>
 F;1/Modified site: acetylated amino end (Met) #status predicted

Query Match 72.0%; Score 486; DB 1; Length 132;
 Best Local Similarity 71.0%; Pred. No. 2.5e-37;
 Matches 93; Conservative 15; Mismatches 23; Indels 0; Gaps 0;
 Qy 1 MCDAFVGFWKLVSSENFDYMKVGVGPATRKVAGMAKPNNMIIISVNGDVITKSESTEFKN 60
 Db 1 MSKFLGFWKLVSSENFDYMKVGVGPATRKVAGMAKPNNMIIISVNGDVITKSESTEFKN 60
 Qy 61 TEISFILQGQFDEVTAADRKVKSITLDDGGVLYHVQKWDGKSTTIKRREDKLUVVECM 120
 Db 61 TEISFILQGQFDEVTAADRKVKSITLDDGGVLYHVQKWDGKSTTIKRREDKLUVVECM 120
 Qy 121 KGTVSTRYER 131
 Db 121 KGTVSTRYER 131

Query Match 70.7%; Score 477; DB 2; Length 133;
 Best Local Similarity 70.2%; Pred. No. 1.7e-36;
 Matches 92; Conservative 11; Mismatches 28; Indels 0; Gaps 0;

Qy 1 MCDAFVGFWKLVSSENFDYMKVGVGPATRKVAGMAKPNNMIIISVNGDVITKSESTEFKN 60
 Db 1 MSKFLGFWKLVSSENFDYMKVGVGPATRKVAGMAKPNNMIIISVNGDVITKSESTEFKN 60
 Qy 61 TEISFILQGQFDEVTAADRKVKSITLDDGGVLYHVQKWDGKSTTIKRREDKLUVVECM 120
 Db 61 TEISFILQGQFDEVTAADRKVKSITLDDGGVLYHVQKWDGKSTTIKRREDKLUVVECM 120
 Qy 121 KGTVSTRYER 131
 Db 121 KGTVSTRYER 131

RESULT 5
 A27452 fatty acid-binding protein - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 15-Dec-1988 #sequence_change 13-Aug-1999
 C;Accession: A28456; A23138; A39551; A28197; S06478; S02471
 R;Heuckeroth, R.O.; Birkennmeier, E.H.; Leytin, M.S.; Gordon, J.I.
 J. Biol. Chem. 262, 9789-9717, 1987
 A;Title: Analysis of the tissue-specific expression, developmental regulation, and linka
 A;Reference number: A28458; MUID:87250640
 A;Accession: A28458
 A;Molecule type: mRNA
 A;Residues: 1-133 <HEU>
 A;Cross references: GB:J02773; NID:g204077; PID:AAA41136.1; PID:g204078
 R;Clafferty, K.P.; Herrera, V.L.; Brecher, P.; Ruiz-Opazo, N.
 Biochemistry 26, 7900-7904, 1987
 A;Title: Cloning and tissue distribution of rat heart fatty acid binding protein mRNA:
 A;Reference number: A27452; MUID:88107756
 A;Accession: A27452
 A;Molecule type: mRNA
 A;Residues: 1-133 <CLA>
 A;Cross references: GB:MI8034; NID:g204079; PID:AAA41137.1; PID:g204080
 A;Experimental source: heart
 R;Sacchettini, J.C.; Said, B.; Schulz, H.; Gordon, J.I.
 J. Biol. Chem. 261, 8218-8223, 1986
 A;Title: Rat heart fatty acid-binding protein is highly homologous to the murine adipocyt
 A;Reference number: A23838; MUID:862250713
 A;Accession: A23838
 A;Molecule type: protein
 A;Residues: 'TEKN', 5-50, 'YG', 53-64, 'N', 65-70, 'D', 72-133 <SAC>
 A;Experimental source: heart
 R;Kimura, H.; Odani, S.; Nishi, S.; Sato, H.; Arakawa, M.; Ono, T.
 J. Biol. Chem. 266, 5963-5972, 1991
 A;Title: Primary structure and cellular distribution of two fatty acid-binding proteins
 A;Reference number: A39551; MUID:91170283
 A;Accession: A39551
 A;Stratus: preliminary
 A;Molecule type: protein
 A;Residues: 10-69, 'Q', 71-121, 'D', 123-133 <KIM>
 A;Experimental source: kidney
 R;Gibson, B.W.; Yu, Z.; Aberth, W.; Burlingame, A.L.; Bass, N.M.
 J. Biol. Chem. 263, 4182-4185, 1988
 A;Title: Revision of the blocked N terminus of rat heart fatty acid-binding protein by
 A;Reference number: A28197; MUID:88153733
 A;Accession: A28197
 A;Molecule type: protein
 A;Residues: 2-10; 46-53 <GTB>

RESULT 6
 PC011 fatty acid-binding protein - mouse (fragment)
 C;Species: Mus musculus (house mouse)
 C;Date: 29-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 13-Aug-1999
 C;Accession: PC4011; S04591; S02278; PC1248
 R;Treuner, M.; Kozaik, C.A.; Gallahan, D.; Grossae, R.; Mueller, T.
 Gene 14, 237-242, 1994
 A;Title: Cloning and characterization of the mouse gene encoding mammary-derived grow
 A;Reference number: PC4011; MUID:95011621
 A;Accession: PC4011
 A;Molecule type: mRNA
 A;Residues: 1-133 <TR>
 A;Cross references: GB:U02884; NID:9409956; PID:AAA61933.1; PID:9409957
 R;Tweedie, S.; Edwards, Y.
 Nucleic Acids Res. 17, 4374, 1989
 A;Title: cDNA sequence for mouse heart fatty acid binding protein, H-FABP.
 A;Reference number: S04591
 A;Accession: S04591
 A;Molecule type: mRNA
 A;Residues: 1-33, 'G', 35-98, 'D', 100-133 <TWE>
 A;Cross references: ENBL:XI4961; NID:951266; PID:951267
 R;Tweedie, S.; Edwards, Y.
 submitted to the EMBL Data Library, April 1989
 A;Accession: S05278
 A;Molecule type: mRNA
 A;Residues: 1-2, 'ER', 5-33, 'G', 35-98, 'D', 100-133 <TW2>
 A;Cross references: ENBL:X4961
 A;Experimental source: cardiac
 R;Bansal, M.P.; Medina, D.
 Biochem. Biophys. Res. Commun. 191, 61-69, 1993
 A;Title: Expression of fatty acid-binding proteins in the developing mouse mammary g

Db	1	MSNFKLGDTWKLVSSENFDYKKALGGGLATRKLNLAQKPTVIIISKGDDITTRTESTFKN	60
QY	61	TEISFILGQEFDEVTAADDRKVSTITLDGGYLVHQWDKGKSTTICKREDDDKLYVECM	120
	61	11111: : : : : : : : : : :	
Db	61	TEISFKLGQEFFETADNRKTSVTLQRGSNLNQVRWDGKETTICKRLVNGKMAECKM	120
QY	121	KGYTSTRYER	131
	121	: :	
Db	121	KSYVCTRUYEK	131
RESULT			
JH0407	8		
myelin P2 protein - mouse			
C:	Species: <i>Mus musculus</i> (house mouse)		
C:	Date: 31-Dec-1991 #sequence_revision	31-Dec-1991	#text_change 13-Aug-1991
C:	Accession: JH0407		
R:	Narayanan, V.; Kaestner, K.H.; Tennekoop, G.T.		
J. Neurochem.	57, 75-80, 1991		
A:	Title: Structure of the mouse myelin P2 protein gene.		
A:	Reference number: JH0407; MU0:91268811		
A:	Accession: JH0407		
A:	Molecule type: DNA		
A:	Residues: 1-132 <NAR>		
A:	Cross-references: GR:539508; NID:932319; PIIN:AA019249;1; PID:932320		
C:	Comment: This basic protein is found in peripheral and central nervous s		
C:	Genetics:		
A:	Introns: 25/1; 82/3; 116/3		
C:	Family: myelin P2 protein		

A;Title: Characterization and amino acid sequence of a fatty acid-binding protein from bovine heart muscle
 A;Reference number: S00603; MUID:88339972
 A;Accession: S00603
 A;Molecule type: protein
 A;Residues: 2-104; 'K',106-124, 'S',126-133 <OFF>
 A;Note: Submitted to the Protein Sequence Database, May 1988
 R;Zanotti, G.; Scapin, G.; Spadon, P.; Veerkamp, J.H.; Sacchettini, J.C.
 J. Biol. Chem. 267: 18541-18550, 1992
 A;Title: Three-dimensional structure of recombinant human muscle fatty acid-binding protein
 A;Reference number: A4251; MUID:92406763
 A;Contents: annotation: X-ray crystallography, 2.1 angstroms
 A;Note: recombinant protein expressed in Escherichia coli
 R;Troxier, R.F.; Ofner, G.D.; Jiang, J.W.; Wu, B.L.; Skare, J.C.; Milunsky, A.; Wyandt, J.M.; Genet. 92: 563-566, 1993
 A;Title: Localization of the gene for human heart fatty acid binding protein to chromosome 15
 A;Reference number: 154275; MUID:94085553
 A;Accession: I54275
 A>Status: translated from GB/EMBL/DDJB
 A;Molecule type: mRNA
 A;Residues: 15-133 <RES>
 A;Cross-references: GB:S67314; NID:9458861; PIDN:AAB29294.1; PID:9458862
 A;Gene: GDB:FABP3
 A;Cross-references: GDB:128608; OMIM:134651
 A;Map position: 1p33 -1p32
 C;Superfamily: myelin P2 protein
 C;Keywords: acetylated amino end; cardiac muscle; heart; lipid binding; phosphoprotein
 F;2/Modified site: acetylated amino end (Val) (in mature form) #status experimental
 F;20/Binding site: phosphate (Tyr) (covalent) #status predicted
 F;127,129/Binding site: fatty acid (Arg, Tyr) #status experimental

Query	Match	Score	Length	DB	Indels	Gaps
Qy	1 MCDAFGTWKLVSSENDDYMKEVGYGPFATRKVAGMAKPNMIIISVNGDVITIKSESTFKN	66.5%	449;	1;	0;	0;
Matches	Best Local Similarity 64.9%; Pred. No. 5.9e-34; Conservative 85; Mismatches 16; Indels 0; Gaps 0;					
Db	1 MVDAFLGTWKLVDSKNEDDYMKLSLGIVGPFATRKVAGMAKPNMIIISVNGDVITIKSESTFKN	60				
Qy.	61 TEISFLGQEFDETADDRKYKSTIITLDGVLYHQWDKGKSTIKRKEDDKLIVVECYM	120				
Db	61 TEISFLGQEFDETADDRKYKSTIITLDGVLYHQWDKGKSTIKRKEDDKLIVVECYM	120				
Qy	121 KGVTSPTRYER 131					
Db	121 GTAVCTRTYEK 131					

RESULT 10

MPBO2
 myelin P2 protein - bovine
 C;Species: Bos primigenius taurinus (cattle)
 C;Date: 31-Aug-1980 #sequence_revision 31-Aug-1980 *text_change 05-Aug-1994
 C;Accession: A03144
 R;Kitamura, K.; Suzuki, A.; Uyemura, K.
 FEBS Lett. 115: 27-30, 1980
 A;Title: The complete amino acid sequence of the P2 protein in bovine peripheral nerve
 A;Reference number: A03144; MUID:80225120
 A;Accession: A03144
 A;Molecule type: protein
 A;Residues: 1-131 <KIT>
 C;Superfamily: myelin P2 protein
 C;Keywords: acetylated amino end
 F;1/Modified site: acetylated amino end (Ser) #status experimental
 F;117-124/Disulfide bonds: #status experimental

Query	Match	Score	Length	DB	Indels	Gaps
Qy	5 FVGTVKLVSSENDDYMKEVGYGPFATRKVAGMAKPNMIIISVNGDVITIKSESTFKN	66.4%	448;	1;	0;	0;
Matches	Best Local Similarity 67.7%; Pred. No. 7.1e-34; Conservative 86; Mismatches 25; Indels 0; Gaps 0;					

Qy 121 KGVTSSTRYER 131
 Db 121 GTAVCTRTYEK 131

RESULT 12
 S06479 fatty acid-binding protein, brain - bovine
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992
 C;Accession: S06479; JH0198
 R;Schoentgen, F.; Pignede, G.; Bonanno, L.M.; Jolles, P.
 R; Biochim. 185, 35-40, 1989
 A;Title: Fatty-acid-binding protein from bovine brain. Amino acid sequence and some properties
 A;Reference number: S06479; MUID:90032683
 A;Accession: S06479
 A;Molecule type: protein
 A;Residues: 1-131 <SCH>
 A;Experimental source: brain
 A;Note: 11-Val, 12-Asp, 14-Lys, 18-Asp, 33-Ala, 34-Ser, 40-Thr, 43-Glu, 44-Lys, 49-Val,
 R;Schoentgen, F.; Bonanno, L.M.; Pignede, G.; Jolles, P.
 Mol. Cell. Biochem. 98, 35-39, 1990
 A;Title: Amino acid sequence and some ligand binding properties of fatty acid-binding protein
 A;Reference number: JH0198; MUID:91094811
 A;Contents: annotation
 C;Superfamily: synaptosomal Na⁺-dependent amino acid transport is stimulated by the fatty acid
 C;Keywords: blocked amino end (Val) (probably acetylated) #status experimental
 F;1/Modified site: blocked amino end (Val) myelin P2 protein

Query Match 63.0%; Score 425; DB 2; Length 131;
 Best Local Similarity 62.0%; Pred. No. 8.8e-32;
 Matches 80; Conservative 20; Mismatches 29; Indels 0; Gaps 0;

Qy 3 DAFVGTVKLVSSENDDYMKKEYGVGFATRKVAGMAKPNNMISVNGDVITIKSESTFKN 62
 Db 2 DAFVGTVKLVSSENDDYMKKEYGVGFATRKVAGMAKPNNMISVNGDVITIKSESTFKN 61

Qy 63 ISFILGQEFDETTADRKVKSTITLDGGVLVHQWKDGKSTIKRKREDDKLVVECMKG 122
 Db 62 ISFILGQEFDETTADRKVKSTITLDGGVLVHQWKDGQESLYREMVGKLILTLTHGD 121

Qy 123 VTSTRYER 131
 Db 122 VVAVRYEK 130

RESULT 13
 A49184 fatty acid-binding protein - chicken
 N;Alternative names: Lipid-binding protein
 C;Species: Gallus gallus (chicken)
 C;Accession: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 13-Aug-1999
 C;Accession: A49184; S26599
 R;Godbout, R.
 EXP: Eye Res. 56, 95-106, 1993
 A;Title: Identification and characterization of transcripts present at elevated levels i
 A;Reference number: A49184; MUID:93162137
 A;Status: Preliminary
 A;Molecule type: mRNA
 R;Residues: 1-132 <SCH>
 A;Cross-references: EMBL:X65459; NID:g63230; PID:CAA46451_1; PID:g63233
 A;Experimental source: retina
 R;Note: sequence extracted from NCBI backbone (NCBIP:124757)
 C;Superfamily: myelin P2 protein

Query Match 58.1%; Score 392; DB 2; Length 132;
 Best Local Similarity 56.1%; Pred. No. 8.9e-29;
 Matches 74; Conservative 19; Mismatches 39; Indels 0; Gaps 0;

Qy 1 MCDAFGTVKLVSSENDDYMKKEYGVGFATRKVAGMAKPNNMISVNGDVITIKSESTFKN 60
 Db 1 MVEAFCATWKLADSHNFDEMKAIGVGFAMRQ/GNVTKTVTISSEGDKVVKRIVQSTFKN 60

Qy 61 TEISFILGQEFDETTADRKVKSTITLDGGVLVHQWKDGKSTIKRKREDDKLVVECM 120
 Db 61 TEISFILGQEFDETTADRKVKSTITLDGGVLVHQWKDGKETNFVREIKDGRMVMTLTF 120

Qy 121 KGVTISTRYERA 132
 Db 121 GDVYAVRYHEK 132

RESULT 14
 I52524 testis lipid binding protein - rat
 A;Alternate names: 15 kDa perforin-like protein, PERF 15
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 13-Aug-1999
 C;Accession: I52524; I55089
 R;Schmitt, M.C.; Jamison, R.S.; Orgebin-Crist, M.C.; Ong, D.E.
 Biol. Reprod. 51, 239-245, 1994
 A;Title: A novel, testis-specific member of the cellular lipophilic transport protein
 A;Reference number: I52524; MUID:95035569
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-132 <RES>
 A;Cross-references: EMBL:U07870; NID:g469051; PID:AAA68627_1; PID:g469052
 R;Oko, R.J.; Morales, C.C.; Oko, R.; Morales, C.R.
 Dev. Biol. 166, 235-245, 1994
 A;Title: A novel testicular protein, with sequence similarities to a family of lipid
 A;Accession number: I53089; MUID:95046505
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-132 <RES>
 A;Cross-references: EMBL:U09022; NID:g538268; PID:AAA67873_1; PID:g538269
 C;Superfamily: myelin P2 protein

Query Match 57.8%; Score 390; DB 2; Length 132;
 Best Local Similarity 56.5%; Pred. No. 1.4e-28;
 Matches 74; Conservative 26; Mismatches 31; Indels 0; Gaps 0;

Qy 1 MCDAFGTVKLVSSENDDYMKKEYGVGFATRKVAGMAKPNNMISVNGDVITIKSESTFKN 60
 Db 1 MIEPLGLTVKLVSSENDDYMKKEYGVGFATRKVAGMAKPNNMISVNGDVITIKSESTFKN 60

Qy 61 TEISFILGQEFDETTADRKVKSTITLDGGVLVHQWKDGKSTIKRKREDDKLVVECM 120
 Db 61 TEISFILGQEFDETTADRKVKSTITLDGGVLVHQWKDGKETNFVREIKDGRMVMTLTF 120

Qy 121 KGVTISTRYER 131
 Db 121 NNVSTRYER 131

RESULT 15
 I56510 fatty acid binding protein - rat
 C;Species: Rattus norvegicus (Norway rat)
 C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 13-Aug-1999
 C;Accession: I56510
 R;Bennett, E.; Stevens, K.L.; Lund, P.K.; Popko, B.
 J. Neurochem. 63, 1616-1624, 1994
 A;Title: Cloning and characterization of a cDNA encoding a novel fatty acid binding protein
 A;Reference number: I56510; MUID:95016702
 A;Accession: I56510
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: mRNA
 A;Residues: 1-132 <RES>

A;Cross-references: EMBL:002096; NID:9476081; PIDN:AAA60455.1; PID:g476082
C;Superfamily: myelin P2 protein

Query Match	57.0%	Score 385;	DB 2;	Length 132;
Best Local Similarity	55.3%	Pred. No. 3.9e-28;		
Matches 73;	Conservative 19;	Mismatches 40;	Indels 0;	Gaps 0;
Qy 1 MCDAFYGTVKLVSSSEENDDYMKVEVGFAIRKVGAMAKPAMISNGDVITIKSSTEFKN 60				
Db 1 MVDACATWKLTDSQNFDENMKAALGVGFATRQGNVTKPVYIISQEGGKVVRQCTFKN 60				
Qy 61 TEISFLQQBDEVTADEKKVKSITILDGGVLVHVQKWDGKSTTIKRREDDKLIVECYM 120				
Db 61 TEISFOLQGEFEETSIDDRNCKSVTRLDGKLIHVQKWDGKRETNCVREIKDGRMVTLRF 120				
Qy 121 KGVTSRVYER 132				
Db 121 GDVVAVRCTEK 132				

search completed: January 24, 2002, 09:16:01
Job time: 123 sec

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QY 2 CDAFGTQKLVSSENNDDYMKKEVGVGPFATRKVAGMAKPNMISVNGDVITIKSESTFKNT 61
 DB 1 CDAFGTQKLVSSENNDDYMKKEVGVGPFATRKVAGMAKPNMISVNGDVITIKSESTFKNT 60

QY 62 EISFILQEQDEVTADDKYKSTITLGGYLVHYQKWDGKSTTIKRKREDDKLVVECYMK 121
 DB 61 EISFILQEQDEVTADDKYKSTITLGGYLVHYQKWDGKSTTIKRKREDDKLVVECYMK 120

QY 122 GVTSTRYERA 132
 DB 121 GVTSTRYERA 131

RESULT 2
 FABA MOUSE STANDARD; PRT; 131 AA.

AC P04177;
 DT 01-NOV-1986 (Rel. 03, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE FATTY ACID-BINDING PROTEIN, ADIPOCYTE (AFABP) (ADIPOCYTE LIPID-BINDING PROTEIN) (ALBP) (P2 ADIPOCYTE PROTEIN) (MYELIN P2 PROTEIN HOMOLOG) (3T3 LL LIPOPID BINDING PROTEIN) (422 PROTEIN) (P15).
 GN FABP4 OR AP2.
 OS Mus musculus (Mouse).
 OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus; NCBI_TaxID=10090; RN [1]

RP SEQUENCE FROM N.A. MEDLINE=8623319; PubMed=3520554;
 RX Bernlohr D.A., Angus C.W., Lane M.D., Bolanowski M.A., Kelly T.J. Jr.; RA "Expression of specific mRNAs during adipose differentiation: identification of an mRNA encoding a homologue of myelin P2 protein." RT Proc. Natl. Acad. Sci. U.S.A. 81:5468-5472(1984).
 RN [2]
 RP SEQUENCE FROM N.A. MEDLINE=8623319; PubMed=3520554;
 RX Phillips M., Dobson D.E., Min H.Y., Spiegelman B.M.; RA "Adipocyte P2 gene: developmental expression and homology of 5'-flanking sequences among fat cell-specific genes." RT Proc. Natl. Acad. Sci. U.S.A. 83:3786-3790(1986).
 RN [3]
 RP SEQUENCE FROM N.A. MEDLINE=86278164; PubMed=3015443;
 RX Phillips M., Djian P., Green H.; RA "The nucleotide sequence of three genes participating in the adipose differentiation of 3T3 cells." RT J. Biol. Chem. 261:10821-10827(1986).
 RN [4]
 RP SEQUENCE OF 1-10 FROM N.A. MEDLINE=89008309; PubMed=2844775;
 RX Matarese V., Bernlohr D.A.; RA "Purification of murine adipocyte lipid-binding protein. Characterization as a fatty acid- and retinoic acid-binding protein." RT J. Biol. Chem. 263:14544-14551(1988).
 RN [5]
 RP SEQUENCE OF 10-131 FROM N.A. MEDLINE=85105214; PubMed=3968175;
 RX Cook K.S., Hunt C.R., Spiegelman B.M.; RA "Developmentally regulated mRNAs in 3T3-adipocytes: analysis of transcriptional control." RT J. Cell Biol. 100:514-520(1985).

RN [7] X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 MEDLINE=922073; PubMed=1554730.
 RX Xu Z., Bernlohr D.A., Banaszak L.J.; RA "The adipocyte lipid-binding protein at 1.6-A resolution. Crystal structures of the apoprotein and with bound saturated and unsaturated fatty acids." RT J. Biol. Chem. 268:7874-7884(1993).
 RL PRT X-RAY CRYSTALLOGRAPHY (1.6 ANGSTROMS).
 RX MEDLINE=9216758; PubMed=846311;
 RA Xu Z., Bernlohr D.A., Banaszak L.J.; RT "The adipocyte lipid-binding protein at 1.6-A resolution. Crystal structures of the apoprotein and with bound saturated and unsaturated fatty acids." RL J. Biol. Chem. 268:7874-7884(1993).
 CC -1- FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG CHAIN FATTY ACID AND RETINOIC ACID.
 CC -1- SUBCELLULAR LOCALIZATION: CRYPTOPLASMIC (POTENTIAL).
 CC -1- SIMILARITY: BELONGS TO THE FABP/P2/CRABP FAMILY OF TRANSPORTERS.
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 CC -1- DR EMBL; K02109; AAA39416; 1;
 DR EMBL; M13264; AAA39870; 1;
 DR EMBL; M1261; AAA39870; 1; JOINED.
 DR EMBL; M1262; AAA39870; 1; JOINED.
 DR EMBL; M1263; AAA39870; 1; JOINED.
 DR EMBL; M1385; AAA39417; 1;
 DR EMBL; M20497; AAA37188; 1;
 DR EMBL; M28126; AAA37112; 1;
 DR PIR; A05089; A05089;
 DR PIR; A24884; A24884;
 DR PIR; A30810; A30810;
 DR PIR; B25952; B25952;
 DR PDB; 1ALB; 31-OCT-93.
 DR PDB; 1L1C; 30-APR-94.
 DR PDB; 1L1D; 30-APR-94.
 DR PDB; 1L1E; 30-APR-94.
 DR PDB; 1L1F; 30-APR-94.
 DR PDB; 1ADL; 20-DEC-94.
 DR PDB; 1ABO; 16-JUN-97.
 DR PDB; 1ACD; 16-JUN-97.
 DR PDB; 1A1B; 01-JUL-98.
 DR SWISS-2DPAGE; P04117; MOUSE.
 DR MGII; MGII-88038; AP2.
 DR InterPro; IPR000463; Fatty_acid_BP.
 DR InterPro; IPR000566; Lipocin_cytfABP.
 DR Pfam; PF00061; Lipocalin; 1.
 DR PRINTS; PR00178; FATTYACIDBP.
 DR PROSITE; PS00114; FABP; 1.
 KW Transport; Lipid_Binding; Phosphorylation; 3D-structure.
 FT INIT MET 0 0
 FT MOD_RES 19 19 PHOSPHORYLATION (BY TYR_KINASES)
 FT (BY SIMILARITY).
 FT CONFLICT 39 39 N->T (IN REF. 2;
 FT CONFLICT 110 110 G->V (IN REF. 3; AAA39417).
 FT HELIX 2 4
 FT STRAND 6 14
 FT HELIX 16 23
 FT TURN 24 24
 FT HELIX 27 35
 FT STRAND 39 45
 FT TURN 46 47
 FT STRAND 48 54

FT STRAND 59 64
 FT TURN 66 67
 FT STRAND 70 73
 FT TURN 75 76
 FT STRAND 79 87
 FT TURN 88 89
 FT STRAND 90 97
 FT TURN 98 99
 FT STRAND 100 109
 FT TURN 110 111
 FT STRAND 112 119
 FT TURN 120 121
 FT STRAND 122 130
 SQ SEQUENCE 131 AA; 14519 MW; ED57D4E2774B8E32 CRC64;

Query Match 91.9%; Score 620; DB 1; Length 131;
 Best Local Similarity 91.6%; Pred. No. 7.2e-49;
 Matches 120; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 2 CDAFVGTVKLVSSSENFDDMKKEYGVGFEATRKVAGMAKDNMISVNGDVITIKSESTFANT 61
 Db 1 CDAFVGTVKLVSSSENFDDMKKEYGVGFEATRKVAGMAKDNMISVNGDLVTIRSESTFANT 60

QY 62 EISPLQGEDEDEVTAADDKVKSITLTDGGSVLYVQKWDGKSITTKRKEDDKLIVVECVMK 121.
 Db 61 EISPLQGEDEDEVTAADDKVKSITLTDGGSVLYVQKWDGKSITTKRKEDDKLIVVECVMK 120

QY 122 GTISTRYERA 132
 Db 121 GTISTRYERA 131

RESULT_ 3
 FABP_PIG STANDARD; PRT; 131 AA.
 AC O97788;
 DT 20-AUG-2001 (Rel. 40, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE FATTY ACID-BINDING PROTEIN, ADIPOCYTE (AFABP) (ADIPOCYTE LIPID-BINDING PROTEIN) (ALBP) (A-FABP) (AP2).
 GN FABP4.
 CS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 RN [1]
 RP SEQUENCE FROM N.A., AND CHARACTERIZATION.
 RX STRAIN-DUROC; TISSUE=Liver;
 RX MEDLINE=990989248; PubMed=980671;
 RA Gerbens F, Jansen A., van Erp A.J.M., Harders F., Meuwissen T.H.E.,
 RA Reitmeijer G.F.W., Veerkamp J.H., te Pas M.F.W.;
 RR "The adipocyte fatty acid-binding protein locus: characterization and association with intramuscular fat content in pigs.";
 RR Mamm. Genome 9:1022-1026(1998).
 RN [2]
 RP SEQUENCE OF 36-47, AND TISSUE SPECIFICITY.
 RC TISSUE=Fat;
 RX MEDLINE=90241143; PubMed=2334399;
 RA Armstrong M.K., Bernlohr D.A., Storch J., Clarke S.D.;
 RR The purification and characterization of a fatty acid binding protein specific to pig (Sus domesticus) adipose tissue. *J. Biomed. Biochem.* J. 267:373-378(1990).

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 CC EMBL: Y16039; CAA73995; 1; -
 DR HSP; P04117; LIID.
 DR InterPro; IPR000463; Fatty acid BP.
 DR InterPro; IPR000566; Lipocalin_cytfABP.
 Pfam; PF00061; Lipocalin; 1.
 DR PRINTS; PRO0178; FATTYACIDDBP.
 DR PROSITE; PS00214; FABP; 1.
 KW Transport; Lipid-binding; Phosphorylation.
 FT INTR-MET 0 0 BY SIMILARITY.
 MOD_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES)
 (BY SIMILARITY).
 SQ SEQUENCE 131 AA; 14545 MW; 636CB0A08CD4AB2 CRC64;
 Query Match 90.1%; Score 608; DB 1; Length 131;
 Best Local Similarity 88.5%; Pred. No. 8.4e-48;
 Matches 116; Conservative 9; Mismatches 6; Indels 0; Gaps 0;
 QY 2 CDAFVGTVKLVSSSENFDDMKKEYGVGFEATRKVAGMAKDNMISVNGDVITIKSESTFANT 61
 Db 1 CDAFVGTVKLVSSSENFDDMKKEYGVGFEATRKVAGMAKDNMISVNGDLVTIRSESTFANT 60
 QY 62 EISPLQGEDEDEVTAADDKVKSITLTDGGSVLYVQKWDGKSITTKRKEDDKLIVVECVMK 121
 Db 61 EISPLQGEDEDEVTAADDKVKSITLTDGGSVLYVQKWDGKSITTKRKEDDKLIVVECVMK 120
 RESULT_ 4
 FABP_RAT STANDARD; PRT; 131 AA.
 ID FABP_RAT
 AC P70623;
 AC P70623;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE FATTY ACID-BINDING PROTEIN, ADIPOCYTE (AFABP) (ADIPOCYTE LIPID-BINDING PROTEIN) (ALBP).
 DE PROTEIN (ALBP).
 GN FABP4.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RN MAMMALIA; NCBI_TAXID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Prinsen C., Veerkamp J.H.;
 RA Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 CC FUNCTION: LIPID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG CHAIN FATTY ACID AND RETINOIC ACID.
 CC SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
 CC SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF TRANSPORTERS.
 CC
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 CC EMBL: U75581; AAB18344; 1; -
 DR

DR HSSP; P04117; 1ALB.
DR InterPro; IPR000463; Fatty acid BP.
DR InterPro; IPR000566; Lipocalin_cytFABP.
DR Pfam; PF00061; Lipocalin; 1.
DR PRINTS; PR00178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
DR Transport; Lipid-binding; phosphorylation.
KW transport; Lipid-binding; phosphorylation.
INIT MET 0
MOD_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES)
BY SIMILARITY.
FT MW 5228D0AC14FFD23B CRC64;
SEQUENCE 131 AA; 14577 MW; 5228D0AC14FFD23B CRC64;

Query Match 89.9%; Score 607; DB 1; Length 131;
Best Local Similarity 88.5%; Pred. No. 1e-47; Indels 0; Gaps 0;
Matches 116; Conservative 8; Mismatches 7; Standard 131 AA.

QY 2 CDAFVGTWKLVSSNFDDYMKVEYGFAFRKVAGMAKPNNMISYNGDVITIKSESTFKNT 61
DB 1 CDAFVGTWKLVSSNFDDYMKVEYGFAFRKVAGMAKPNNMISYNGDVITIKSESTFKNT 60

QY 62 EISFLGQEFDETTADDRKVSKITLDGGYLHVQKWDGSKTTIKRKREDDKLVVECYMK 121
DB 61 EISFLGQEFDETTADDRKVSKITLDGGYLHVQKWDGSKTTIKRKREDDKLVVECYMK 120

QY 122 GVTSTRYERA 132
DB 121 GVTSTRYERA 131

RESULT 6
MYP2_RABBIT
ID MYP2_RABBIT
STANDARD
PRT: 131 AA.

AC P02631;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE MYELIN P2 PROTEIN.
OS Oryctolagus cuniculus (Rabbit).
OCAukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OC NCBI_TaxID=9386;
RN [1] SEQUENCE FROM N.A.
RN MEDLINE=80094496; PubMed=2453513;
RN RA "The NH2-terminal region of the P2 protein from rabbit sciatic nerve
RT myelin".
RN [2] SEQUENCE OF 1-55.
RN MEDLINE=88228063; PubMed=7356651;
RN RA "Mammary derived growth inhibitor is not a distinct protein but a mix
RT of heart-type and adipocyte-type fatty acid-binding protein.";
RN J. Biol. Chem. 271:19943-19948 (1996).
CC -1- FUNCTION: LIQUID TRANSPORT PROTEIN IN ADIPOCYTES. BINDS BOTH LONG
CC SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
CC TRANSPORTER.

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CC or send an email to license@isb-sib.ch).

CC DR EMBL; X8944; CAA61532; 1;
CC DR HSSP; P04117; 1A2D.
CC DR InterPro; IPR00463; Fatty_acid_BP.
CC DR InterPro; IPR000566; Lipocalin_cytFABP.
CC DR Pfam; PF00061; Lipocalin; 1.
CC

DR PRINTS; PRO0178; FATTYACIDBP.
DR PROSITE; PS00214; FABP; 1.
DR Transport; Lipid-binding; Phosphorylation.
FT INIT_MET 0
FT MOD_RES 19 19 BY SIMILARITY.
FT PHOSPHORYLATION (BY TYR-KINASES)
FT (BY SIMILARITY).
SQ SEQUENCE 131 AA; 14547 MW; A7D81B036C972D68 CRC64;

Query Match 84.9%; Score 573; DB 1; Length 131;
Best Local Similarity 84.0%; Pred. No. 1.e-44;
Matches 110; Conservative 8; Mismatches 13; Indels 0; Gaps 0;

QY 2 CDAFVGTWKLVSSNFDDYMKVEYGFAFRKVAGMAKPNNMISYNGDVITIKSESTFKNT 61
DB 1 CDAFVGTWKLVSSNFDDYMKVEYGFAFRKVAGMAKPNNMISYNGDVITIKSESTFKNT 60

QY 62 EISFLGQEFDETTADDRKVSKITLDGGYLHVQKWDGSKTTIKRKREDDKLVVECYMK 121
DB 61 EISFLGQEFDETTADDRKVSKITLDGGYLHVQKWDGSKTTIKRKREDDKLVVECYMK 120

QY 122 GVTSTRYERA 132
DB 121 GVTSTRYERA 131

RESULT 6
MYP2_RABBIT
ID MYP2_RABBIT
STANDARD
PRT: 131 AA.

AC P02631;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1989 (Rel. 11, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE MYELIN P2 PROTEIN.
OS Oryctolagus cuniculus (Rabbit).
OCAukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OC NCBI_TaxID=9386;
RN [1] SEQUENCE FROM N.A.
RN MEDLINE=80094496; PubMed=2453513;
RN RA "The NH2-terminal region of the P2 protein from rabbit sciatic nerve
RT myelin".
RN [2] SEQUENCE OF 1-55.
RN MEDLINE=88228063; PubMed=7356651;
RN RA "Mammary derived growth inhibitor is not a distinct protein but a mix
RT of heart-type and adipocyte-type fatty acid-binding protein.";
RN J. Biol. Chem. 271:19943-19948 (1996).
CC -1- FUNCTION: THIS PROTEIN MAY BE A LIQUID TRANSPORT PROTEIN IN SCHWANN
CC CELLS.
CC -1- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER
CC CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN
CC PROTEIN.
CC -1- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
CC TRANSPORTERS.

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CC PRELIMINARY SEQUENCE.
 CC MEDLINE=86250713; PubMed=2424895;
 DR RX
 DR RA Sacchettini J.C., Said B.J., Schulz H., Gordon J.I.;
 PIR; A03145; MPB2;
 PIR; A28081; A28081.
 DR RT "Rat heart fatty acid-binding protein is highly homologous to the
 murine adipocyte P2 protein and the P2 protein of peripheral nerve
 myelin";
 DR RT
 DR RL J. Biol. Chem. 261:8218-8223(1986).
 DR RN [5]
 DR RN
 DR RN
 DR RC TISSUE=Kidney;
 DR RX MEDLINE=911702B3; PubMed=2005132;
 RN RA Kimura H., Odani S., Nishi S.-I., Sato H., Arakawa M., Ono T.;
 RN RT "Primary structure and cellular distribution of two fatty
 acid-binding proteins in adult rat kidneys.";
 RN RT
 RN RL J. Biol. Chem. 266:5963-5972(1991).
 RN RN [6]
 RN RP SEQUENCE OF 58-96.
 RN RX MEDLINE=893774061; PubMed=2775193;
 RN RA Kimura H., Hitomi M., Odani S., Koide T., Arakawa M., Ono T.;
 RN RT "Rat heart fatty acid-binding protein. Evidence that supports the
 amino acid sequence predicted from the cDNA.";
 RN RL Biochem. J. 260:303-306(1989).
 RN RN [7]
 DR RC PARTIAL SEQUENCE.
 DR RX MEDLINE=90032682; PubMed=2806260;
 DR RA Kanda T., Iseki S., Hitomi M., Kimura H., Kondo H.,
 DR RA Matsubara Y., Moto T., Ono T.,
 DR RT "Purification and characterization of a fatty-acid-binding protein
 from the gastric mucosa of rats. Possible identity with heart
 fatty-acid-binding protein and its parietal cell localization.";
 DR RL Eur. J. Biochem. 185:7-13(1989).
 DR RN [8]
 DR RN PARTIAL SEQUENCE.
 DR RC TISSUE=Mammary gland;
 DR RX MEDLINE=88326235; PubMed=3415652;
 DR RA Jones P.D., Carne A., Bass N.M., Grigor M.R.;
 DR RT "Isolation and characterization of fatty acid binding proteins from
 rat mammary tissue of lactating rats.";
 DR RL Biochem. J. 251:919-925(1988).
 DR RN [9]
 DR RC PARTIAL SEQUENCE.
 DR RX MEDLINE=94162301; PubMed=8117746;
 DR RA Nielsen S.U., Rump R., Hoeijrup P., Roepstorff P., Spener F.,
 DR RT "Differentiation, regulation and phosphorylation of the fatty acid-
 binding protein from rat mammary epithelial cells.";
 DR RL Biochim. Biophys. Acta 1211:189-197(1994).
 DR CC "-1- FUNCTION: FABP ARE THOUGHT TO PLAY A ROLE IN THE INTRACELLULAR
 TRANSPORT OF LONG-CHAIN FATTY ACIDS AND THEIR ACYL-COA ESTERS.
 DR CC "-1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 DR CC "-1- TISSUE SPECIFICITY: HEART, BUT ALSO SKELETAL MUSCLE, KIDNEY,
 DR CC "-1- BRAIN AND MAMMARY GLAND.
 DR CC "-1- SIMILARITY: BELONGS TO THE FABP/P2/CRBP FAMILY OF
 DR TRANSPORTERS.
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 DR CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 DR or send an email to license@isb-sib.ch).
 DR EMBL J02773; AAA41136_1;
 DR DR EMBL M18034; AAA41137_1;
 DR PIR; A236338; A23838;
 DR PIR; A27452; A27452;
 DR PIR; A28197; A28197;
 DR PIR; A28458; A28458;
 DR PIR; A39551; A39551;
 DR PIR; S06478; S06478;
 DR HSSP; P05413; 2HMB.

RESULTS
 7
 FABP_RAT STANDARD; PRT; 132 AA.
 ID P07433;
 AC 01-APR-1988 (Rel. 07, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DE 01-FBB-1996 (Rel. 33, Last annotation update)
 DE FATTY ACID-BINDING PROTEIN, HEART (H-FABP).
 GN FABP.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RN MEDLINE=87250640; PubMed=3036869;
 RA Henckeroth R.O., Birkenmeier E.H., Levin M.S., Gordon J.I.;
 RT "Analysis of the tissue-specific expression, developmental
 regulation, and linkage relationships of a rodent gene encoding heart
 fatty acid binding protein".
 RL J. Biol. Chem. 262:9709-9717(1987).
 RN SEQUENCE FROM N.A.
 RN MEDLINE=88107756; PubMed=3427112;
 RA Claffey K.P., Herrera V.L., Brecher P., Ruiz-Opazo N.;
 RT "Cloning and tissue distribution of rat heart fatty acid-binding
 protein mRNA: identical forms in heart and skeletal muscle.";
 RT Biochemistry 26:7900-7904(1987).
 RN [3]
 RP SEQUENCE.
 RX MEDLINE=88153733; PubMed=3162235;
 RA Gibson B.W., Yu Z., Abert W., Burlingame A.L., Bass N.M.;
 RT "Revision of the blocked N terminus of rat heart fatty acid-binding
 protein by liquid secondary ion mass spectrometry.";
 RL J. Biol. Chem. 263:4182-4185(1988).
 RN

DR InterPro; IPR000463; Fatty_acid_BP.
 DR InterPro; IPR000566; Lipocln_cytFABP.
 DR PF0061; Lipocalin; 1.
 DR PRINTS; PR00178; FATTYACIDBP.
 DR PROSITE; PS00214; FABP; 1.
 DR PROTEIN; Lipid-binding; Acetylation; Phosphorylation.
 KW TRANSPORT; Lipid-binding; Acetylation; Phosphorylation.
 FT INIT_MET 0 0
 FT MOD_RES 1 1 ACETYLATION.
 FT MOD_RES 19 1 PHOSPHORYLATION (BY TYR-KINASES).
 FT CONFLICT 63 63 S -> SN (IN REF. 3).
 FT CONFLICT 69 69 E -> Q (IN REF. 5).
 FT CONFLICT 70 70 F -> D (IN REF. 3).
 SQ SEQUENCE 132 AA; 14643 MW; 31B4C66A8BFBA5BE CRC64;

Query Match 69.9%; Score 472; DB 1; Length 132;
 Best Local Similarity 70.5%; Pred. No. 1.2e-35;
 Matches 91; Conservative 11; Mismatches 27; Indels 0; Gaps 0;
 PRT; 131 AA.

Qy 3 DAFYGWTWKLYSENFDYYMKKEVGYGFATRKVAGWAKPNMITSVNGDVTRIKSESTEFKNTNE 62
 Db 2 DAFYGWTWKLYSDKNEDYYMKMSLGIVGFAVRYASMTKPTTIEKGDTTIKTHSTFKNTNE 61

Qy 63 ISFIUQEFDEVTDADDKVKSTITLDGGVLSKTKREDDKLVVECMKG 122
 Db 62 ISFOLGVEEFDEVTDADDKVKSSVTLDGGKLHVQKWDGQETTLRELSDGKLILTLHGN 121

Qy 123 VTSTRYER 131
 Db 122 VVS TRYEK 130

RESULT 8
 FABP_MOUSE STANDARD; PRT; 132 AA.
 ID FABP_MOUSE ;
 AC P11404 ;
 DT 01-JUL-1989 (Rel. 11, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE FATTY ACID-BINDING PROTEIN, HEART (H-FABP) (MAMMARY-DERIVED GROWTH INHIBITOR) (MDG1).
 GN FABP3 OR FABPH1.
 OS Mus musculus (Mouse).
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murine; Mus; NCBI_TAXID=10050;
 OX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6 X CBA;
 RA MEDLINE=89396486; PubMed=2740224;
 RA Tweedie S.; Edwards Y.;
 RA "CDNA sequence for mouse heart fatty acid binding protein, H-FABP.";
 RN [2]
 RP REVISIONS TO 2-3.
 RA Tweedie S.;
 RA Submitted (AUG-1989) to the EMBL/GenBank/DDBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ICR SWISS; TISSUE=Liver;
 RX MEDLINE=95011621; PubMed=7926807;
 RA Treuner M., Kozak C.A., Gallahan D., Grosse R., Mueller T.;
 RT "Cloning and characterization of the mouse gene encoding mammary-derived growth inhibitor/heart-fatty acid-binding protein."
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=Mammary gland;
 RX MEDLINE=93054235; PubMed=429305;
 RA Binas B., Spitzer E., Zschiesche W., Erdmann B., Kurtz A., Mueller T., Niemann C., Bleau W., Grosse R.;
 RA "Hormonal induction of functional differentiation and mammary-derived growth inhibitor expression in cultured mouse mammary gland"

RT explants.";
 RL In Vitro Cell. Dev. Biol: 28A:625-634(1992).
 CC -I- FUNCTION: FABP ARE THOUGHT TO PLAY A ROLE IN THE INTRACELLULAR TRANSPORT OF LONG-CHAIN FATTY ACIDS AND THEIR ACYL-COA ESTERS.
 CC -I- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -I- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF TRANSPORTERS.
 CC --FT This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC --FT DR CAA31084; 1;
 DR EMBL; X14968; 1;
 DR EMBL; U02883; AAA0345; 1;
 DR PIR; S04591; S04591;
 DR HSP; P05413; 2HMB.
 DR SWISS-2DPAGE; P11404; MOUSE.
 DR MGI; MGI-95476; Fabp3.
 DR InterPro; IPR000463; Fatty_acid_BP.
 DR InterPro; IPR00566; Lipocalin_cytFABP.
 DR Pfam; PF00061; Lipocalin_1.
 DR PROSITE; PS0214; FABP; 1.
 DR Transport; Lipid-binding; Acetylation; Phosphorylation.
 FT INIT_MET 0 0 ACETYLATION (BY SIMILARITY).
 FT MOD_RES 1 1 PHOSPHORYLATION (BY TYR-KINASES).
 FT MOD_RES 19 19 (BY SIMILARITY).
 FT CONFLICT 33 33 A -> G (IN REF. 1).
 FT CONFLICT 98 98 D -> N (IN REF. 3 AND 4).
 SQ SEQUENCE 132 AA; 14689 MW; F73B8E6DAC1AB6A CRC64;

Query Match 69.0%; Score 466; DB 1; Length 132;
 Best Local Similarity 69.0%; Pred. No. 4.1e-35;
 Matches 89; Conservative 14; Mismatches 26; Indels 0; Gaps 0;
 PRT; 131 AA.

Qy 3 DAFYGWTWKLYSENFDYYMKKEVGYGFATRKVAGWAKPNMITSVNGDVTRIKSESTEFKNTNE 62
 Db 2 DAFYGWTWKLYSDKNEDYYMKMSLGIVGFAVRYASMTKPTTIEKGDTTIKTHSTFKNTNE 61

Qy 63 ISFILUQEFDEVTDADDKVKSTITLDGGVLSKTKREDDKLVVECMKG 122
 Db 62 INFQLGIEFDEVTDADDKVKSSVTLDGGKLHVQKWDGQETTLRELSDGKLILTLHGS 121

Qy 123 VTSTRYER 131
 Db 122 VVS TRYEK 130

RESULT 9
 MYP2_HUMAN STANDARD; PRT; 131 AA.
 ID MYP2_HUMAN
 AC P02689;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE MYELIN_P2 PROTEIN.
 GN PMP2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OC NCBI_TAXID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9206819; PubMed=1720307;
 RA Hayasaka K., Nanno K., Tahara M., Sato W., Takada G., Miura M., Uemura K.;

"Isolation and sequence determination of cDNA encoding P2 protein of human peripheral myelin.";
 RT Biochem. Biophys. Res. Commun. 181:204-207(1991).
 RN [2]
 RP SEQUENCE.
 RX MEDLINE=83058785; PubMed=6183401;
 RA Suzuki M.; Kitamura K.; Sakamoto Y.; Uyemura K.;
 "The complete amino acid sequence of human P2 protein.";
 RL J. Neurochem. 39:1759-1762(1982).
 RN [3]
 RP SEQUENCE OF 1-115 FROM N.A.;
 MEDLINE=95054012; PubMed=7525873;
 RA Narayanan V.; Ripepi B.; Jabs E.W.; Hawkins A.; Griffin C.;
 TNennekotter G.;
 RT "Partial structure and mapping of the human myelin P2 protein gene.";
 RL J. Neurochem. 63:2010-2013(1994).
 CC -I- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN CELLS.
 CC -I- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN PROTEIN.
 CC -I- SIMILARITY: BELONGS TO THE FABP/P2/CRABP FAMILY OF TRANSPORTERS.
 CC -----
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 DR EMBL; D16181; BAA03726.1;
 DR EMBL; D16179; BAA03726.1; JOINED.
 DR EMBL; D16180; BAA03726.1; JOINED.
 DR EMBL; X62167; CAA44096.1; -.
 DR EMBL; S73470; AAB32599.2; -.
 DR EMBL; S73468; AAB32592.2; JOINED.
 DR EMBL; S73469; AAB32592.2; JOINED.
 DR PIR; A03143; MPH02.
 DR HSSP; P02690; 1PMP.
 DR MIM; 170715; -.
 DR InterPro; IPR00463; Fatty_acid_BP.
 DR InterPro; IPR000566; Lipocalin_cytFABP.
 DR Pfam; PF00061; Lipocalin; 1.
 DR PRINTS; PR00176; FATTYACIDBP.
 DR PROSITE; PS00214; FABP; 1.
 KW Myelin; Lipid-binding; Transport; Acetylation.
 DR INIT_MET 0
 FT MOD_RES 1
 FT DISULFID 117 124
 FT 24 24
 FT G > GG (IN REF. 3).
 FT CONFLICT 98 98
 FT D > N (IN REF. 2).
 FT CONFLICT 110 110
 FT N > D (IN REF. 2).
 SQ SEQUENCE 131 AA; 14778 MW; 3D0E640BA03E63D2 CRC64;

RESULT 10
 MYP2_BOVIN STANDARD; PRT; 131 AA.
 ID MYP2_BOVIN
 AC P02690;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE MYELIN P2 PROTEIN.
 GN PMP2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
 OC Bovidae; Bovinae; Bos.
 OC NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=80225120; PubMed=6156092;
 RA Kitamura K.; Suzuki M.; Suzuki A.; Uyemura K.;
 RT "The complete amino acid sequence of the P2 protein in bovine peripheral nerve myelin.";
 RL FEBS Lett. 115:27-30(1980).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RX MEDLINE=89005045; PubMed=2458918;
 RA Jones T.A.; Bergfors T.; Sedzik J.; Unge T.;
 RT "The three-dimensional structure of P2 myelin protein.";
 RL EMBO J. 7:1597-1604(1988).
 RN [3]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RX MEDLINE=93353783; PubMed=7683727;
 RA Cowan S.W.; Newcomer M.E.; Jones T.A.;
 RT "Crystallographic studies on a family of cellular lipophilic transport proteins. Refinement of P2 myelin protein and the structure determination and refinement of cellular retinol-binding protein in complex with all-trans-retinol.";
 RL J. Mol. Biol. 230:1225-1246(1993).
 CC -I- FUNCTION: THIS PROTEIN MAY BE A LIPID TRANSPORT PROTEIN IN SCHWANN CELLS.
 CC -I- MISCELLANEOUS: P2 PROTEIN AND MYELIN BASIC PROTEIN TOGETHER CONSTITUTE A MAJOR FRACTION OF PERIPHERAL NERVOUS SYSTEM MYELIN PROTEIN.
 CC -I- SIMILARITY: BELONGS TO THE FABP/P2/CRABP FAMILY OF TRANSPORTERS.
 CC PIR; A03144; MBPO2.
 DR PDB; 1PMP; 26-JAN-95.
 DR InterPro; IPR000653; Fatty_acid_BP.
 DR Pfam; PF00061; lipocalin; 1.
 DR PRINTS; PR0176; FATTYACIDBP.
 DR PROSITE; PS00214; FABP; 1.
 KW Myelin; Lipid-binding; Transport; Acetylation; 3D-structure.
 FT MOD_RES 1
 FT DISULFID 117 124
 SQ SEQUENCE 131 AA; 14818 MW; 1424AAF386EA0B21 CRC64;

Query Match 66 4%; Score 448; DB 1; Length 131;
 Best Local Similarity 67.7%; Pred. No. 1.6e-33;
 Matches 86; Conservative 16; Mismatches 25; Indels 0; Gaps 0;
 Qy 5 FVGTWKLVSSENFDYMKKEYGAGRKVKAGMARNMISVNGDVITIKSESTKNTIELS 64
 4 FLGTWKLVSSENFDYMKALKGVGLATRKLNALKPTVILTRTESTKNTIELS 63
 Qy 65 FILGQEFDEVADDEKKVKSTTLDDGVLVHVKQNDGKSTTIKRREDDKLVECMKGVT 124
 64 FKLGQEFEEFTADNRKTKS1VTLORGSLNQVRMDGKETTIKRKLVNGRMVAECRMKGTV 123
 Qy 125 STRYER 131
 Db 124 CTRIYEK 130

RE	MEDLINE=95006319; PubMed=7922029;	Query Match	65.9%;	Score 445;	DB 1;	Length 132;
RA	Young A.C.M., Seapin G., Kromminga A., Patel S.B., Veerkamp J.H., Sacchettini J.C.;	Best Local Matches	65.1%;	Pred. No. 3.1e-33;		
RA	"Structural studies on human muscle fatty acid binding protein at 1.4-A resolution: binding interactions with three C18 fatty acids.";	Matches	84;	Conservative	16;	Mismatches 0;
RT	FUNCTION: FABP ARE THOUGHT TO PLAY A ROLE IN THE INTRACELLULAR TRANSPORT OF LONG-CHAIN FATTY ACIDS AND THEIR ACYL-OO ESTERS.	Qy	3 DAFVGWKLVSSENFDYMDKEVGVGFATRKVAGMAKPNMITSVNGDVITIKSESTFKNTE 62			
RL	-!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF TRANSPORTERS.	Db	2 DAFLGTWKLVDSKNFDMKSLGVGFATRQAVASMTKPTTIEKNGDILTKTHSFKNTE 61			
CC	-!- SIMILARITY: CYTOPLASMIC.	Qy	63 ISFTLQQEFDVETTADEKKVSTITLDGIVLYHQWDGKSTTIKKRDEDKLVLVCEVMKGS 122			
CC	-!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF TRANSPORTERS.	Db	62 ISFKLVEFDTTADRKVSIVTLGKLVHLQWDGQETTLVRELIDGKLILITHGTT 121			
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CC	EMBL; X56549; CAA39899.1;	FABH_BOVIN	STANDARD;	PRT;	132 AA.	
DR	EMBL; Y10245; CAA71305.1;	ID	FABH_BOVIN			
DR	EMBL; U57623; AAB02555.1;	AC	P10790; P12103;			
DR	EMBL; U17081; AAC99800.1;	DT	01-JUL-1989 (Rel. 11, Created)			
DR	EMBL; S67314; AAB29294.1;	DT	01-JUL-1989 (Rel. 11, Last sequence update)			
DR	PIR; S00663; FABHUC.	DT	20-AUG-2001 (Rel. 40, Last annotation update)			
DR	PIR; JH0193; JH0199.	DE	FATTY ACID-BINDING PROTEIN, HEART (H-FABP) (MAMMARY-DERIVED GROWTH INHIBITOR) (MDG).			
DR	PIR; S15432; S15432.	DE	DE			
DR	PDB; 1HMR; 08-MAY-95.	GN	FABP3.			
DR	PDB; 1HMS; 08-MAY-95.	OS	Bos taurus (Bovine)			
DR	PDB; 1HMT; 08-MAY-95.	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
DR	PDB; 2HMB; 31-JAN-94.	OC	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;			
DR	HSC-2NPAGE; P05413; HUMAN	OC	Bovidae; Bovinae; Bos.			
DR	MIM: 134651;	OX	NCBI-Taxid=9913;			
DR	InterPro; IPR000463; Fatty_acid_BP.	RN	[1]			
DR	InterPro; IPR000566; Lipocin_cytFFABP.	RP	SEQUENCE FROM N.A.			
DR	Pfam; PF00061; Lipocalin_1.	RX	Medline=8811264; PubMed=3409882;			
DR	PRINTS; PR00178; FATTYACIDBP.	RA	Billlich S., Wissel T., Kratzin H., Hahn U., Hagenhoff B.,			
DR	PROSITE; PS0024; FABP.	RA	Lezius A.G., Spener F.;			
RW	Transport; Lipid-binding; Acetylation: Phosphorylation; 3D-structure.	RT	"Cloning of a full-length complementary DNA for fatty-acid-binding protein from bovine heart."			
FT	INIT_MET	RT	RL			
FT	MOD_RES	RT	UR. J. Biochem. 175:549-556(1988).			
FT	MOD_RES	RN	[2]			
FT	MOD_RES	SEQUENCE.	RN			
FT	MOD_RES	RX	Medline=90375486; PubMed=2398054;			
FT	MOD_RES	RA	Unterberg C., Boerchers T., Hoejrup P., Roepstorff P., Knudsen J.,			
FT	MOD_RES	RA	Spener F.			
FT	MOD_RES	RA	"Cardiac fatty acid-binding proteins. Isolation and characterization of the mitochondrial fatty acid-binding protein and its structural relationship with the cytosolic isoforms."			
FT	MOD_RES	RT	J. Biol. Chem. 265:16255-16261(1990).			
FT	MOD_RES	RT	[3]			
FT	MOD_RES	RN	RN			
FT	MOD_RES	RP	SEQUENCE FROM N.A.			
FT	MOD_RES	RC	TISSUE=Mammary gland.			
FT	MOD_RES	RX	Medline=90233786; PubMed=2335570;			
FT	MOD_RES	RA	Boehmer F.-D., Kraft R., Otto A., Wernstedt C., Hellman U., Kurtz A.,			
FT	MOD_RES	RA	Mueller T., Rohde K., Etzold G., Lehmann W., Langen P., Heldin C.-H.,			
FT	MOD_RES	RA	Grosse R.;			
FT	MOD_RES	RT	"Identification of a polypeptide growth inhibitor from bovine mammary gland. Sequence homology to fatty acid- and retinoid-binding proteins."			
FT	MOD_RES	RT	J. Biol. Chem. 262:15137-15143(1987).			
FT	MOD_RES	RL	[5]			
FT	MOD_RES	RN	RN			
FT	MOD_RES	RP	SEQUENCE OF 1-131.			
FT	MOD_RES	RX	Medline=88033096; PubMed=3667628;			
FT	MOD_RES	RA	Boehmer F.-D., Kraft R., Otto A., Wernstedt C., Hellman U., Kurtz A.,			
FT	MOD_RES	RA	Mueller T., Rohde K., Etzold G., Lehmann W., Langen P., Heldin C.-H.,			
FT	MOD_RES	RA	Grosse R.;			
FT	MOD_RES	RT	"Identification of a polypeptide growth inhibitor from bovine mammary			
FT	MOD_RES	RT	gland. Sequence homology to fatty acid- and retinoid-binding			
FT	MOD_RES	RL	proteins."			
FT	MOD_RES	RN	J. Biol. Chem. 262:15137-15143(1987).			
FT	MOD_RES	RP	[5]			
FT	MOD_RES	RC	SEQUENCE.			
FT	MOD_RES	RX	Medline=9416156; PubMed=8312397;			
FT	MOD_RES	RA	Zabari M., Berri M., Rouchou P., Zamora F., Tassy C.,			
FT	SEQUENCE	RA	Ribadeau-Dumas B., Quail A.;			

"Purification and characterisation of a polymorphic low Mr bovine muscle cysteine proteinase inhibitor: structural identity with fatty-acid-binding proteins." Biochimie 75: 937-945 (1993).

[6] VARIANT IN POSITION 98. MEDLINE=93358876; PubMed=8354262; Bartetzko N., Lexius A.G., Spener F.; "Isoforms of fatty-acid-binding protein in bovine heart are coded by distinct mRNA"; Eur. J. Biochem. 215:555-559 (1993).

[7] X-RAY CRYSTALLOGRAPHY. MEDLINE=91301134; PubMed=2070787; Mueller-Fahrnow A., Egner U., Jones T.A., Ruedel H., Spener F., Saenger W.; "Three dimensional structure of fatty-acid-binding protein from bovine heart.;" Eur. J. Biochem. 199:271-276 (1991).

[8] STRUCTURE BY NMR. MEDLINE=93130916; PubMed=1483473; Luecke C., Lassen D., Kreikenkamp H.-J., Spener F., Rueterjans H.; "Sequence-specific ¹H-NMR assignment and determination of the secondary structure of bovine heart fatty-acid-binding protein." Eur. J. Biochem. 210:901-910 (1992).

[7] STRUCTURE BY NMR.
MEDLINE=95324534; Lassen D., Leueck C., Kveder M., Mesgarzadeh A., Schmidt J.M., Spect B., Lezius A., Spener F., Rueterians H.; "Three-dimensional structure of bovine heart fatty-acid-binding protein with bound palmitic acid, determined by multidimensional NMR spectroscopy." Eur. J. BioChem. 230:266-280(1995).

[10] STRUCTURE BY NMR.
MEDLINE=98149696; Mesgarzadeh A., Pfeiffer S., Engelke J., Lassen D., Rueterians H.; "Bound water in apo and holo bovine heart fatty-acid-binding protein determined by heteronuclear NMR spectroscopy." Eur. J. Biochem. 251:771-786(1999).

-!- FUNCTION: FABP ARE THOUGHT TO PLAY A ROLE IN THE INTRACELLULAR

- 1 - FUNCTION: MDG1 REVERSIBLY INHIBITS PROLIFERATION OF MAMMARY CARCINOMA CELLS.
- 1 - SUBCELLULAR LOCATION: CYTOPLASMIC OR MITOCHONDRIAL MATRIX.
- 1 - TISSUE SPECIFICITY: MAMMARY EPITHELIAL CELLS OF DEVELOPING LOBULOALVEOLAR STRUCTURES AND HEART.
- 1 - SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF TRANSPORTERS.

CC EMBL; X12710; CAA31212; 1;
 EMBL; X51933; CAA36199; 1;
 PIR; A29466; A29466;
 PIR; S01133; S01133;
 PIR; A34676; A34676;
 PIR; A37883; A37883;
 PDB; 1BXY; 07-OCT-98.
 InterPro; IPR00463; Fatty_acid_BP.
 InterPro; IPR00566; Lipocalin_cytFABP.
 Pfam; PF00061; lipocalin; 1.
 PRINTS; PS00178; FATTYACIDBP.
 DR Transport; Lipid-binding; Acetylation; Phosphorylation; 3D-structure.
 DR Transport; Lipid-binding; Acetylation; Phosphorylation; 3D-structure.
 KWW

	INIT_MET	0	0	ACETYLATION.
FT	MOD_RES	1	19	PHOSPHORYLATION (BY TYR-KINASES)
FT	MOD_RES	19	19	(BY SIMILARITY).
FT	VARIANT	98	98	N -> D.
FT	CONFLICT	12	14	DSK -> SSE (IN REF. 4).
FT	CONFLICT	40	43	T -> L (IN REF. 4).
FT	CONFLICT	43	43	E -> S (IN REF. 4).
FT	CONFLICT	93	93	H -> Q (IN REF. 4).
FT	CONFLICT	127	127	T -> V (IN REF. 4).
SO	SEQUENCE	132 AA:	14648 MW:	(65204932C6DFD35 CRC64:

CC -> FUNCTION: ENZYME THAT IS INVOLVED IN THE TRANSPORT OF LONG-CHAIN FATTY ACIDS AND THEIR ACYL-COA ESTERS.
CC -> SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -> SIMILARITY: BELONGS TO THE FABP/P2/CRBPP/CRABP FAMILY OF TRANSPORTERS.

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CC -----.
DR EMBL: X98558; CA67168.1; - .
DR HSSP: P10790; 1BHY.
DR IPR00463; Fatty_acid_BP.
DR InterPro; IPR00556; Lipocin_cytfabP.
DR Pfam: PF00061; lipocalin; 1.
DR PRRTMS; PRQ0178; FattyAcIDBP.
DR PROSITE; PS00214; FABP;
DR

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KW Transport; Lipid-binding; Acetylation; Phosphorylation.
 FT INIT_MET 0 0
 FT MOD_RES 1 1 BY SIMILARITY.
 FT MOD_RES 19 19 ACETYLATION (BY SIMILARITY).
 FT MOD_RES 19 19 PHOSPHORYLATION (BY TYR-KINASES) (BY
 SIMILARITY).
 SQ SEQUENCE 132 AA; 14618 MW; B5431E65EF596C95 CRC64;

Query Match 65.5%; Score 442; DB 1; Length 132;
 Best Local Similarity 65.1%; Pred. No. 5.7e-33; Indels 0; Gaps 0;
 Matches 84; Conservative 15; Mismatches 30; Indels 0; Gaps 0;

Qy 3 DAFVGTWKLVSSENFDYMKEVGVGFATRKVAGMAKPNMITSVNGDVITKSESTEKFNTE 62
 Db 2 DAFAGTWKLVDSKNFDDYMGSIGVFAIROVANMKPTILEVNGDTIITKTQSTFKESTE 61
 Qy 63 ISFLIGQEEFDETTADDRKVKSITLDGGKLVHQLQWNGQOPTLVRLEVDKLILTHGS 122
 Db 62 ISFKLGQEEFDETTADDRKVKSITLDGGKLVHQLQWNGQOPTLVRLEVDKLILTHGS 121
 Qy 123 VTSTRYER 131
 |||:
 Db 122 AVCTRYEK 130
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 RESULT 15
 FABP_BOVIN ID FABP_BOVIN STANDARD PRT; 131 AA.
 AC Q09139;
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DE FATTY ACID-BINDING PROTEIN, BRAIN (B-FABP).
 GN FABP.
 CS Bos taurus (Bovine).
 CC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Bovidae; Bovine; Bos.
 CX NCBI_TAXID=9915;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=91094811; PubMed=21266968;
 RA Schoenigen F., Bonanno L.M., Pignede G., Jolles P.;
 RT "Amino acid sequence and some ligand binding properties of fatty
 acid-binding protein from bovine brain.";
 RT Mol. Cell. Biochem. 98:35-39(1990).
 RN [2]
 RP SEQUENCE.
 RC TISSUE=Brain;
 RX MEDLINE=90032683; PubMed=2806261;
 RA Schoenigen F., Pignede G., Bonanno L.M., Jolles P.;
 RT "Fatty-acid-binding protein from bovine brain. Amino acid sequence
 and some properties";
 RL Eur. J. Biochem. 185:35-40(1989).
 CC -I- FUNCTION: FABP ARE THOUGHT TO PLAY A ROLE IN THE INTRACELLULAR
 CC TRANSPORT OF LONG CHAIN FATTY ACIDS AND THEIR ACYL COA ESTERS.
 CC -I- SUBUNIT: MONOMER.
 CC -I- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -I- SIMILARITY: BELONGS TO THE FABP/P2//CRBP FAMILY OF
 CC TRANSPORTERS.
 DR InterPro; IPR00463; Fatty_acid_BP.
 DR InterPro; IPR00566; Lipocalin_CytFABP.
 PFam; PF00061; Lipocalin_1.
 PRNTS; PR00178; FattyAcIDBP.
 PROSITE; PS00244; FABP; 1.
 DR Transport; Lipid-binding.
 KW VARIANT 11 12 TE -> VD.
 FT VARIANT 14 14 Q -> K.
 FT VARIANT 18 18 E -> D.
 FT VARIANT 33 34 GN -> AS.
 FT VARIANT 40 40 L -> T.

Query Match 63.0%; Score 425; DB 1; Length 131;
 Best Local Similarity 62.0%; Pred. No. 1.9e-31; Indels 0; Gaps 0;
 Matches 80; Conservative 20; Mismatches 29; Indels 0; Gaps 0;
 Qy 3 DAFVGTWKLYSSENFDYMKEVGVGFATRKVAGMAKPNMITSVNGDVITKSESTEKFNTE 62
 Db 2 DAFVGTWKLYSSENFDYMKEVGVGFATRKVAGMAKPNMITSVNGDVITKSESTEKFNTE 61
 Qy 63 ISFLIGQEEFDETTADDRKVKSITLDGGKLVHQLQWNGQOPTLVRLEVDKLILTHGS 122
 Db 62 ISFLIGQEEFDETTADDRKVKSITLDGGKLVHQLQWNGQOPTLVRLEVDKLILTHGS 121
 Qy 123 VTSTRYER 131
 |||:
 Db 122 VVAVRHYEK 130
 Search completed: January 24, 2002, 09:18:21
 Job time: 178 sec

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OM protein - protein search, using sw model

Run on: January 24, 2002, 09:15:43 ; Search time 25.01 Seconds
(without alignments)
772.009 Million cell updates/sec

Title: US-09-905-235-1
Perfect score: 675
Sequence: 1 MCDAFYGTWKLYSSENFDYY.....KLVVECVMKGVTSRVYERA 132

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues

Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_17:*

- 1: sp_archea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_minc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rabbit:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*

Result No.

Score

Match

Length

DB

ID

Description

Q9dak4 mus musculu
Q9y90 mus sp. 1mg
001812 caenorhabdi
001814 caenorhabdi
09vgm2 drosophila
Q9bmkl echinocuccu
Q9bly5 echinocuccu
002323 caenorhabdi
Q26517 schistosoma
061236 manduca sex
Q9bnk2 echinocuccu
Q57664 rhizophila
Q9bnk3 echinocuccu
Q45035 schistosoma
Q9epc5 mus musculu
Q9din1 mus musculu
Q9nm00 mus musculu
Q45036 schistosoma
Q9ui96 fasciola he
Q9psa5 xenopus lae
Q9phg brachydanio
002324 caenorhabdi
P82980 homo sapien
Q9uas2 fasciola gi

ALIGNMENTS

RESULT 1
ID Q99p60 PRELIMINARY; PRT;
AC Q99p60; PRT;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ADIPOSE-TYPE FATTY ACID-BINDING PROTEIN.
GN FAP4.
OS Spermophilus tridecemlineatus (Thirteen-lined ground squirrel).
OC Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Spermophilus; Rodentia; Sciurognathi; Sciuridae; Sciuinae;
OC NCBI_TaxID=43179;
OX RN [LINE SEQUENCE FROM N.A.
RP Hittel D.S., Storey K.B.;
RT "Differential expression of adipose- and heart-type fatty acid-binding proteins in hibernating ground squirrels.";
RT Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
RL EML: AF327855; AAK0B084.1;
DR SEQNC 132 AA; 14765 MW; FCB14230E34C0708 CRC64;

Query Match 96.4%; Score 651; DB 11; Length 132;
Best Local Similarity 97.0%; Pred. No. 5.1e-50;
Matches 128; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MCDAFVGSTWKLYSSENFDYMEKVGFGTRKVAGMAKPNMITSYNSDVITKSESTEKFN 60
Db 1 MCDAFVGSTWKLYSSENFDYMEKVGFGTRKVAGMAKPNMITSYNSDVITRSESTKFN 60

Qy 61 TETISFLGQEFDEVADDRKVYSTITLDGGYLVHQWDKGKSTTIRKRKEEDDKLVYECVM 120
Db 61 TETISFLGQEFDEVADDRKVYSTITLDGGYLVHQWDKGKSTTIRKRKEEDDKLVYECVM 120

Qy 121 KGVTSTRYERA 132
Db 121 KGVTSTRYERA 132

RESULT 2

Q9R290	PRELIMINARY;	PRT;	150 AA.		FT	NON-TER	1	113	113 AA;	12536 MW;	4C19A538EC897F4F CRC64;
AC Q9R290;					AC	Q9R290;					
DT 01-MAY-2000 (TREMBLrel. 13, Created)					DT	01-MAY-2000 (TREMBLrel. 13, Last sequence update)					
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)					DT	01-JUN-2001 (TREMBLrel. 17, Last annotation update)					
DE ADIPOCYTE LIPID-BINDING PROTEIN.					DE	ADIPOCYTE LIPID-BINDING PROTEIN.					
GN ALBP.					GN	ALBP.					
OS Rattus norvegicus (Rat)					OS	Rattus norvegicus (Rat)					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.					CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.					
NCBI_TAXID=10116;					NCBI_TAXID=10116;	[1]					
RN					RN						
RP SEQUENCE FROM N.A.					RP	SEQUENCE FROM N.A.					
RC STRAIN=SPRAEAGLE_DANLEY; TISSUE=ADIPOSE TISSUE;					RC	STRAIN=WISTAR; TISSUE=HEART;					
RX MEDLINE=93254074; PUBMED=10318917;					RX	MEDLINE=93254074;					
RA Shen W.-J.; Sridhar K.; Bernlohr D.A.; Kraemer F.B.;					RA	Zhang J., Rickers-Haunerland J., Dave I., Haunerland N.H.;					
RT "Interaction of rat hormone-sensitive lipase with adipocyte lipid-binding protein."					RT	"Structure and chromosomal location of the rat gene encoding the heart fatty acid-binding protein."					
RT binding protein;"					RT	Eur. J. Biochem. 266:347-351(1999).					
RL Proc. Natl. Acad. Sci. U.S.A. 96:5528-5532(1999).					RL	EMBL; AF144756; AF144756; AF144756; AF144756;					
DR EMBL; AF144756; AF144756; AF144756; AF144756.					DR	HSSP; P04117; IID.					
DR HSSP; P04117; IID.					DR	InterPro; IPR00463; Fatty_acid_BP.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PFam; PF00056; Lipocalin_1.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PRINTS; PR00178; FATTYACIDBP.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PROSITE; PS00214; FABP; 1.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PROSITE; PS00061; Lipocalin_1.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PRINTS; PR00178; FATTYACIDBP.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PROSITE; PS00214; FABP; 1.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PROSITE; PS00061; Lipocalin_1.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PRINTS; PR00178; FATTYACIDBP.					
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DR InterPro; IPR00463; Fatty_acid_BP.					DR	PRINTS; PR00178; FATTYACIDBP.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PROSITE; PS00214; FABP; 1.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PROSITE; PS00061; Lipocalin_1.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PRINTS; PR00178; FATTYACIDBP.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PROSITE; PS00214; FABP; 1.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PROSITE; PS00061; Lipocalin_1.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PRINTS; PR00178; FATTYACIDBP.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PROSITE; PS00214; FABP; 1.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PROSITE; PS00061; Lipocalin_1.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PRINTS; PR00178; FATTYACIDBP.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PROSITE; PS00214; FABP; 1.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PROSITE; PS00061; Lipocalin_1.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PRINTS; PR00178; FATTYACIDBP.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PROSITE; PS00214; FABP; 1.					
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DR InterPro; IPR00463; Fatty_acid_BP.					DR	PROSITE; PS00061; Lipocalin_1.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PRINTS; PR00178; FATTYACIDBP.					
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DR InterPro; IPR00463; Fatty_acid_BP.					DR	PROSITE; PS00214; FABP; 1.					
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DR InterPro; IPR00463; Fatty_acid_BP.					DR	PRINTS; PR00178; FATTYACIDBP.					
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DR InterPro; IPR00463; Fatty_acid_BP.					DR	PROSITE; PS00061; Lipocalin_1.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PRINTS; PR00178; FATTYACIDBP.					
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DR InterPro; IPR00463; Fatty_acid_BP.					DR	PROSITE; PS00061; Lipocalin_1.					
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DR InterPro; IPR00463; Fatty_acid_BP.					DR	PROSITE; PS00061; Lipocalin_1.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PRINTS; PR00178; FATTYACIDBP.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PROSITE; PS00214; FABP; 1.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PROSITE; PS00061; Lipocalin_1.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PRINTS; PR00178; FATTYACIDBP.					
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DR InterPro; IPR00463; Fatty_acid_BP.					DR	PROSITE; PS00061; Lipocalin_1.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PRINTS; PR00178; FATTYACIDBP.					
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DR InterPro; IPR00463; Fatty_acid_BP.					DR	PROSITE; PS00061; Lipocalin_1.					
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DR InterPro; IPR00463; Fatty_acid_BP.					DR	PROSITE; PS00061; Lipocalin_1.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PRINTS; PR00178; FATTYACIDBP.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PROSITE; PS00214; FABP; 1.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PROSITE; PS00061; Lipocalin_1.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PRINTS; PR00178; FATTYACIDBP.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PROSITE; PS00214; FABP; 1.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PROSITE; PS00061; Lipocalin_1.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PRINTS; PR00178; FATTYACIDBP.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PROSITE; PS00214; FABP; 1.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PROSITE; PS00061; Lipocalin_1.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PRINTS; PR00178; FATTYACIDBP.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PROSITE; PS00214; FABP; 1.					
DR InterPro; IPR00463; Fatty_acid_BP.					DR	PROSITE; PS00061; Lipocalin_1.					

DE HEART-TYPE FATTY ACID-BINDING PROTEIN.		RESULT 7		
GN FABP3.		ID Q9XST5 PRELIMINARY;		
OS Spermophilus tridecemlineatus (Thirteen-lined ground squirrel).		ID Q9XST5; AC Q9XST5; DT 01-NOV-1999 (TREMBL); 12, Created)		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		DT 01-JUN-2001 (TREMBL); 12, Last sequence update)		
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Sciurinae;		DE HEART-TYPE FATTY ACID-BINDING PROTEIN (FRAGMENT).		
OX NCBI_TaxID=43179;		GN FABP3.		
RN [1]		OS Equus caballus (Horse).		
RA Hittel D.S., Storey K.B. ;		EC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
RT "Differential expression of adipose- and heart-type fatty acid-binding		OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.		
RT proteins in hibernating ground squirrels.";		OC NCBI_TaxID=9796;		
RL Submitted (DEC 2000) to the EMBL/GenBank/DDBJ databases.		OX [1]		
DR EMBL; AF327854; AAK08083.1; .		RP SEQUENCE FROM N.A.		
SQ SEQUENCE 133 AA; 14853 MW; 9F6D6F6DB78AE721 CRC64;		SCAAP F.G., Pelsers M.M.A.L., Van der Vusse G.J., Glatz J.F.C. ;		
Query Match 69.3%; Score 468; DB 11; Length 133;		RT "Cloning of equine H-FABP cDNA."		
Best Local Similarity 67.9%; Pred. No. 6.3e-34;		RL Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.		
Matches 89; Conservative 14; Mismatches 28; Indels 0; Gaps 0;		DR AF143950; AAD32219.1; -.		
QY 1 MCDAFVGTVKLVSSSENDDYMKKEYGVGFATRKVAGMAKPNMILISVNGDVITIKSESTFKN 60		DR HSSP; P10790; 1BMY.		
Db 1 MVDASFVGTVKLVDSKNEFDDYMKMSLGVGFAFTRQASMTKPTTIEKRKGDTIILQTQSTFKN 60		DR InterPro; IPR000463; Fatty_acid_BP.		
QY 61 TEISFILGQEFFDETAADDRKVKSSTTLQDGVLVHQVKNDGKSTTIKRRKEDDLVLCVCM 120		DR InterPro; IPR000566; Lipocalin_cytFABP.		
Db 61 TEISFOLGKEFDETAADDRKVKSSTVLQDGKLVHQVKNDGQETTLVRELNDGKLILTLTH 120		DR Pfam; PF00061; lipocalin_1.		
QY 121 KGTVISTRVER 131		DR PRINTS; PRO0178; FATTYACIDBP.		
Db 121 GSVCVTRTEK 131		FT NON_TER 1 1; DR NON_TER 1 1;		
RESULT 6		FT SQ SEQUENCE 125 AA; 13965 MW; 9AF89C6A66B79D71 CRC64;		
Q97675 PRELIMINARY; PRT; 99 AA.		Query Match 63.3%; Score 427; DB 6; Length 125;		
ID 097675 PRELIMINARY; PRT; 99 AA.		Best Local Similarity 66.7%; Pred. No. 2.3e-30;		
AC 097675; 10. Created)		Matches 82; Conservative 13; Mismatches 28; Indels 0; Gaps 0;		
DT 01-MAY-1999 (TREMBL); 10, Last sequence update)		QY 9 WKLYSSENEDDYMEKVGIVGFATRKVAGMAKPNMILISVNGDVITIKSESTFKNTEISFLIG 68		
DT 01-JUN-2001 (TREMBL); 17, Last annotation update)		Db 1 WKLVDSKNFDDYMKSIGTGFATROVNNTKPTTIEVNGDTIKTHETEKFNTEISFLIG 60		
DE ADIPOCYTE FATTY ACID BINDING PROTEIN (FRAGMENT).		QY 69 QEEFBVTAADDKRKVKSSTTLQDGVLVHQVKNDGKSTTIKRRKEDDLVLCVCMGVTSPR 128		
GN AP2.		Db 61 VEFDDETTADDRKVKSSTVLQDGKLVHQVKNDGQETTLVRELNDGKLILTLTHSAVSPRT 120		
OS scrofa (Pig).		QY 129 YER 131		
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		Db 121 YEK 123		
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.		RESULT 8		
OX NCBI_TaxID=9823; [1]		Q9TIN9 PRELIMINARY;		
RN SEQUENCE FROM N.A.		ID Q9IBN9		
RA Ding S.T., Mersmann H.J. ;		AC 09IBN9;		
RL Submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.		DT 01-OCT-2000 (TREMBL); 15, Created)		
DR EMBL; AF02872; AAC78684.1; -.		DR 01-OCT-2000 (TREMBL); 15, Last sequence update)		
DR HSSP; P04117; 1LID.		DT 01-JUN-2001 (TREMBL); 17, Last annotation update)		
DR InterPro; IPR000463; Fatty_acid_BP.		DE BRAIN-TYPE FATTY ACID BINDING PROTEIN		
DR InterPro; IPR000566; Lipocalin_cytFABP.		OS Brachydanio rerio (Zebrafish) (zebra danio).		
DR Pfam; PF00061; lipocalin_1.		OC Actinoperygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;		
DR PRINTS; PRO0178; FATTYACIDBP.		OC Cypriniformes; Cyprinidae; Rasborinae; Danno.		
FT NON_TER 1 1;		OX NCBI_TaxID=7955;		
FT NON_TER 99 99 MW; C1E053304FB18F3E CRC64;		RN [1]		
Q9TIN9 PRELIMINARY;		RP SEQUENCE FROM N.A.		
TISSUE=BRAIN.		RC Denovan-Wright E.M., Pierce M., Wright J.M. ;		
RA Denovan-Wright E.M., Pierce M., Wright J.M. ;		RT "Nucleotide sequence of cDNA clones coding for a brain-typ		
RT "Nucleotide sequence of cDNA clones coding for a brain-typ		binding protein and its tissue-specific expression in adult zebrafish		
RT binding protein and its tissue-specific expression in adult zebrafish		DR BIochim. Biophys. Acta 0:0-(2000).		
RT BIochim. Biophys. Acta 0:0-(2000).		DR AF237712; AAF79948.1;		
RT BIochim. Biophys. Acta 0:0-(2000).		DR InterPro; IPR000463; Fatty_acid_BP.		
RT BIochim. Biophys. Acta 0:0-(2000).		DR InterPro; IPR000566; Lipocalin_cytFABP.		
RT BIochim. Biophys. Acta 0:0-(2000).		DR Pfam; PF00061; lipocalin_1.		
RT BIochim. Biophys. Acta 0:0-(2000).		DR PRINTS; PRO0178; FATTYACIDBP.		

DR	PROSITE; PS00214; FABP; 1.	ED59506C71994C55 CRC64;	Db	1 MIEPFGLWKLISSENNENYVRLGVEEPRKYACLIKPSVTSFNGRMIDQAGSACRN 60
SQ	SEQUENCE 132 AA; 14918 MW;		Qy	61 TEISFILGOEFDDEVADRKVKSTITLDGGVLVHQWDKGKSTIKRREDDKLVVECM 120
	Query Match 61.2%; Score 413; DB 13; Length 132;		Db	61 TEISFILGOEFEETTADRKVKSLITFFBGSMIQVQWLGKQTTIKRIVDGMVVECTM 120
	Best Local Similarity 59.1%; Pred. No. 4.3e-29;		Qy	121 KGVTSTRYER 131
	Matches 78; Conservative 21; Mismatches 33; Indels 0; Gaps 0;		Db	121 NNVVSTRYER 131
			RESULT 10	
			057668 PRELIMINARY; PRT; 133 AA.	
			ID 057668; AC 057668;	
			OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Notophenoiidae; Channichthyidae; Cryodraco.	
			DT 01-JUN-1998 (TREMBlrel. 06, Created) DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update) DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)	
			DE FATTY ACID BINDING PROTEIN H8-ISOFORM. GN H8-FABP.	
			OS Cryodraco antarcticus.	
			OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Notophenoiidae; Channichthyidae; Cryodraco.	
			NCBI_TAXID=36192; OX [1] RN	
			SEQUENCE FROM N.A. TISSUE=HEART VENTRICLE; MEDLINE=98129752; PubMed=9461533; RXA Varda M.E., Londreville R.L., Cashon R.E., Costello L., Sidell B.D.; RT "Two distinct types of fatty acid binding protein are expressed in heart ventricle of Antarctic teleost fishes."; RL Biochem. J. 330:373-382(1998).	
			DR InterPro; IPR000463; Fatty_acid_BP. DR InterPro; IPR000566; Lipocalin_cytRBP. DR InterPro; IPR000566; Lipocalin_1. DR Pfam; PF00061; Lipocalin_1. DR PRINTS; PR00178; FATTYACIDBP. SQ SEQUENCE 133 AA; 15011 MW; 1E691AA2738C75FF CRC64;	
			Query Match 59.3%; Score 400; DB 13; Length 133; Best Local Similarity 58.3%; Pred. No. 6e-28; Indels 0; Gaps 0; Matches 77; conservative 18; Mismatches 37; Delins 0;	
			Qy 1 MCDAFVGTLKVSSENEDDMKEYVGFAFRKVAGMAKPNNMISVNGDVITIKSESTFKN 60	
			Db 1 MVDYFVGTLNKDEKFDMKLLGVGPATRQNVTKTIVKTTISVGDKVTLKTQSKRN 60	
			Qy 61 TEISFILGOEFDDEVADRKVKSTITLDGGVLVHQWDKGKSTIKRREDDKLVVECM 120	
			Db 61 TEISFILGOEFEETTADRKVKSLITFFBGSMIQVQWLGKQTTIKRIVDGMVVECTM 120	
			RESULT 11	
			057667 PRELIMINARY; PRT; 133 AA.	
			ID 057667; AC 057667;	
			DT 01-JUN-1998 (TREMBlrel. 06, Created) DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update) DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)	
			DE FATTY ACID BINDING PROTEIN H8-ISOFORM. GN H8-FABP.	
			OS Chaenocephalus aceratus.	
			OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Neoteleostei;	

OC	Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes;	QY	1 MCDAFVGWKLYSSENNEDDYMKEVGGPATRKVAGMAKPKNMISVNGDVITIKSESTFKN 60
OC	Nothonioidae; Channichthyidae; Chaenocephalus.	Db	1 MVDIFVGWNLKDSKFDYMKLKGVGFATROGVNTPKPTTIIISVEGDKVTLTQSATKN 60
RN	[1]		
RP	SEQUENCE FROM N.A.		
RC	TISSUE=HEART VENTRICLE;		
RX	MEDLINE=98129752; PubMed=9461533;	QY	61 TEISFILQEQFDEVADDRKVKSITILDGGVLVHVKNDGKSTIKRREDDKLVYECVM 120
RA	Vayda M.E.; Londreville R.L.; Cashon R.E.; Costello L.; Sidell B.D.;	Db	61 TEISFKLDEEFDDEVADDRKVKSFTVTDGKLVHTQKNDGKTSVLYEVNGNSLTLLKM 120
RT	"Two distinct types of fatty acid-binding protein are expressed in heart ventricle of Antarctic teleost fishes.";	QY	121 KGVTISTRYERA 132
RR	Biochem. J. 330:375-382(1998).	Db	121 DDVESIRYVKA 132
EMBL	U92448; AAC60356.1; -.		
HSSP	P10790; IBWY.		
DR	InterPro: IPR00463; Fatty acid_BP.		
DR	InterPro: IPR00463; Lipocalin_cytfabP.		
DR	PRINTS: PP00061; Lipocalin; 1.		
DR	PRINTS: PR00178; FATTYACIDBP.		
SQ	SEQUENCE 133 AA; 15024 MW; 85157AA2665658C3 CRC64;		
	RESULT 13		
	057691 PRELIMINARY; PRT; 134 AA.		
	AC 057691; PRELIMINARY; PRT; 134 AA.		
	DT 01-JUN-1998 (TREMBLrel. 06, Created)		
	DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)		
	DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)		
	DE FATTY ACID BINDING PROTEIN H6-ISOFORM.		
	OS Chelonecephalus aceratus.		
	OS Cetodraco antarcticus, and		
	OS Chelonecephalus aceratus.		
	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;		
	OC Actinopterygii; Neopterygii; Teleostei; Buteleoste; Neoteleoste;		
	OC Nototherioidae; Channichthyidae; Perciformes;		
	OC Nototherioidae; Channichthyidae; Cryodraco.		
	OX NCBI_TaxID=36192, 36190;		
	RN [1]		
	RP SEQUENCE FROM N.A.		
	RC TISSUE=HEART VENTRICLE.		
	RA Vayda M.E., Londreville R.L., Cashon R.E., Costello L., Winnard P., Small D.J., Hatch H., Sideell B.D.;		
	RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.		
	DR EMBL; U92443; AAC60351.1; -.		
	DR EMBL; U92442; AAC60350.1; -.		
	DR HSSP; P10790.1BNY.		
	DR InterPro; IPR00463; Fatty_acid_BP.		
	DR InterPro; IPR00066; Lipocalin_cytfabP.		
	DR Pfam; PF00061; Lipocalin; 1.		
	DR PRINTS; PR00178; FATTYACIDBP.		
	DR PROSITE; PS00214; FABP.1.		
	SQ SEQUENCE 134 AA; 151.38 MW; D4CBFC689147A98 CRC64;		
	RESULT 12		
	057670 PRELIMINARY; PRT; 133 AA.		
	AC 057670; PRELIMINARY; PRT; 133 AA.		
	DT 01-JUN-1998 (TREMBLrel. 06, Created)		
	DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)		
	DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)		
	DE FATTY ACID BINDING PROTEIN H6-ISOFORM.		
	GN H8_FABP.		
	OS Gobionotothen gibberifrons.		
	OS Gobionotothen gibberifrons.		
	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;		
	OC Actinopterygii; Neopterygii; Teleostei; Buteleoste; Neoteleoste;		
	OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes;		
	OC Nototherioidae; Nototheriidae; Gobionotothen.		
	NCBI_TAXID=6602;		
	RN [1]		
	RP SEQUENCE FROM N.A.		
	RC TISSUE=HEART VENTRICLE;		
	RX MEDLINE=98129752; PubMed=9461533;	QY 1 MCDAFVGWKLYSSENNEDDYMKEVGGPATRKVAGMAKPKNMISVNGDVITIKSESTFKM 59	
	RR "Two distinct types of fatty acid-binding protein are expressed in heart ventricle of Antarctic teleost fishes.";	Db 1 MVEFVGWKMISSDNEDYMAIGFATROGVNTPKPLVSVDDGFVCLKSQSFK 60	
	RR Biochem. J. 330:375-382(1998).	QY 60 NPETISFILQEQFDEVADDRKVKSITILDGGVLVHVKNDGKSTIKRREDDKLVYECV 119	
	DR EMBL; U92251; AAC60359.1; -.	Db 61 TEIPIKKNEPFEETTADDRKVTKVTVLENGKLVQKOSWDGRETNIEIEDGKLVACI 120	
	DR InterPro: IPR000463; Fatty_acid_BP.	QY 120 MGVTISTRYV 129	
	DR InterPro: IPR00066; Lipocalin_cytfabP.	Db 121 MGDIVIAVRTY 130	
	DR PRINTS: PR00178; FATTYACIDBP.		
	SQ SEQUENCE 133 AA; 14997 MW; 85157AA2738C68C3 CRC64;		
	RESULT 14		
	057669 PRELIMINARY; PRT; 133 AA.		
	AC 057669; PRELIMINARY; PRT; 133 AA.		
	DT 01-JUN-1998 (TREMBLrel. 06, Created)		
	DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)		
	DE FATTY ACID BINDING PROTEIN H6-ISOFORM.		
	GN H8_FABP.		
	OS Notothenia coriiceps neglecta (Black rockcod) (Yellowbelly rockcod).		

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
Acanthopteriophyta; Acanthopteriidae; Perciformes;
Noctoatherioidei; Notothiidae; Nototriidae; Nototriidae.
NCBI_TaxID=8209;
[1]
SEQUENCE FROM N.A.
TISSUE=HEART VENTRICLE;
MEDLINE=98129752; PubMed-9461533;
Vayda M.E., Londrillo R.L., Cashon R.E., Costello L., Sidell B.D.:
"Two distinct types of fatty acid-binding protein are expressed in
heart ventricle of Antarctic teleost fishes."
Biochem. J. 330:375-382 (1998).
EMBL; U02450; AAC00358.1; -;
HSSP; P10790; 1BWW;
InterPro; IPR000433; Fatty_acid_BP.
InterPro; IPR000566; Lipocin_CYTRABP.
PRINTS; PR00061; Lipocalin; 1;
SEQUENCE; PR00178; FATTYCACIDBP;
133 AA; 15008 MW;
851B94538D6E78DE CRC54;
15Q

Query	Match	Score	DB	Length
Query	58.1%	Score 392;	DB 13;	Length 133;
Best Local Similarity	56.8%	Pred. No.	3e-27;	0;
Matches	75;	Conservative	19;	Gaps
		Mismatches	38;	Indels
			0;	
Qy	1 MCDAFVGTVWKLYSSENNDDYMEKEYGKFATRKVAGMAKPNMITSYNGDVITIKSBEFKN	60		
Db	1 MVDVFVGTVNLKDSEKPEYMKLGVFATRGVNYTKPTTISVBGDKVTLKTOSAIKN	60		
Qy	61 TEISFILGOEFDDEVTAADRKVKSTITLDGGYLHVQKWDGKSTTKRREDDKLVVECM	120		
Db	61 TEISFKNEEFDETTADRKVKSFVTYDGGKLVHTQKWDGKETSLSYREVNGNSLTLKM	120		
Qy	121 KGVISTRYYERA	132		
Db	121 KGVESTRYYYERA	132		

RESULT	15		
057666		PRELIMINARY;	PRT; 134 AA.
057666; AC	057666; DT	(TREMBIREL. 06, Created)	
01-JUN-1998	01-JUN-2001	(TREMBIREL. 06, Last sequence update) (TREMBIREL. 17, Last annotation update)	
FATTY ACID BINDING PROTEIN H6-ISOFORM.	H6-FABP.		
GN	OS	Parachaenichthys charcoti.	
OC	OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Acanthopterygii; Percomorphi; Perciformes; Oculiferae; Gobiidae; Gobionellinae; Gobionellini; Gobionellus; Gobionellus	

RN [1] SEQUENCE FROM N.A.
 RP TISSUE=HEART VENTRICLE;
 RC MEDLINE=28129752; PubMed=9461533;
 RX Vaya M.E., Londraville R.L., Cashon R.E., Costello L., Stidell B.D.;
 RA RT "Two distinct types of fatty acid-binding protein are expressed in
 heart ventricle of Antarctic teleost fishes.";
 EMBL: U92447; AAC0355.1;
 HSSP: P10790; 1BWY.
 InterPro: IPR000463; Fatty_acid_BP.
 InterPro: IPR000566; Lipocin_cytfBAPP.
 Pfam: PF00061; Lipocalin; 1.
 PRINTS: PR00178; FattyAcidBP.
 PROSITE: PS00214; FABP; 1.
 SEQUENCE: 134 AA: 15161 MW: D4CBCC689121AFA CRC64;
 SO

Best Local Similarity	55.4%	Pred. No.	3.4e-27;
Matches	72;	Mismatches	34;
	Conservative		Indels
Qy	1	MCDAFVGFTWKLYSSNEDDYMKEVGVGFATRKVAGMAKPNTMISVNGD-VITIKSESTF	
Db	1	MYKEFVGWKMSSDNDDYMKEVGVGFATRKVAGMAIGVCFATRKVGNRPTKPNVYVSDQGPFVQLSQTF	
Qy	60	NTEISFLGQEDEVTAADDRKVKRSTTIDGGVLVHVKWDGKSTTIKRKREDDKLVYEE	
Db	61	TTEIKFKNNEPEFETTADDRKTKVTTLENGKLVQKOSWDGKETHIERIEDDGKLVAKC	
Qy	120	MKGVTSPRYV 129	
Db	121	MGDYIAVRTY 130	

Query	Match	Score	DB	Length
Query	Match	58.1%	Score 392;	DB 13; Length 133;
Best Local Similarity		56.8%	Pred. No. 3e-27;	
Matches 75;	Conservative	19;	Mismatches 38;	Indels 0; Gaps 0;
Qy	1 MCDAFVGTVKLVSSNENDDYMEKEYGVGFATRKVAGMKNMISYNGDVTRIKSESTKFN 60			
Db	1 MVDVFQGINNLKDSEFDETMKKGUVGFATRQGVNTKPTLISVBGDKTQLTKOBAIKN 60			
Qy	61 TEISFILQGFDFEYTADERKVKSTITLDGGVLYHVOKWDGKSTTIKRKREDDKLVYECVM 120			
Db	61 TEISFKLNEEFDETTADDRKVKSFTVDDGGLVHVTQWDGKRETSLYREVGNNSLTTLKM 120			
Qy	121 KGUTSTRVVERA 132			
Db	121 DNGVTSRPPVRA 132			

RESULT	15				
057666	ID	057666	PRELIMINARY;	PRT;	134 AA.
	AC	057666;			
	DT	01-JUN-1998	(TREMBLrel. 06, Created)		
	DT	01-JUN-1998	(TREMBLrel. 06, Last sequence update)		
	DT	01-JUN-2001	(TREMBLrel. 17, Last annotation update)		
	DE	FATTY ACID BINDING PROTEIN H6-ISOFORM			
	GN	H6-FABP.			
	OS	Parachaeenichthys charcoti.			
	OU	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	OC	Actinopterygii; Neopterygii; Teleostei; Buteleosteii; Neoteleostei;			
	OC	Acanthomorpha; Acanthopterygii; Perciformes;			
	OC	Stelliferidae; Stelliferinae; Serranidae; Serraninae; Serranidae;			
	OC	Serraninae; Serranidae; Serranidae; Serranidae; Serranidae;			

RN [1] SEQUENCE FROM N.A.
 RP TISSUE=HEART VENTRICLE;
 RC MEDLINE=28129752; PubMed=9461533;
 RX Vaya M.E., Londraville R.L., Cashon R.E., Costello L., Stidell B.D.;
 RA RT "Two distinct types of fatty acid-binding protein are expressed in
 heart ventricle of Antarctic teleost fishes.";
 EMBL: U92447; AAC0355.1;
 HSSP: P10790; 1BWY.
 InterPro: IPR000463; Fatty_acid_BP.
 InterPro: IPR000566; Lipocin_cytfBAPP.
 Pfam: PF00061; Lipocalin; 1.
 PRINTS: PR00178; FattyAcidBP.
 PROSITE: PS00214; FABP; 1.
 SEQUENCE: 134 AA: 15161 MW: D4CBCC689121AFA CRC64;
 SO